

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1452.89 Seconds

(without alignments)
1028.317 Million cell updates/sec

Title: US-10-035-833a-7074

Perfect score: 41
Sequence: 1 tctcataggtcaaaaaaa.....gtccacaaatagtgtgaat 41

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	339	2	BE925815 QV0-BN04
2	41	100.0	493	3	CA393356 cs3h08.y
3	41	100.0	580	7	W02900 zao4h02.r1
4	40	97.6	585	1	A1536104 xue.p9.F9
5	39.4	96.1	663	5	BU686928 UI-CR-PUI
6	28.4	69.3	958	5	BQ723128 AGENCOURT
7	26.6	64.9	700	8	BH967938 cdg80905.
8	25.8	62.9	406	8	A2139688 SP_0001_A
9	25.4	62.0	666	9	BX237182 Danilo rer
10	25.4	62.0	797	9	BX185474 Danilo rer
11	25.2	61.5	765	8	BH524372 BOHMD73TR
12	25.2	61.5	793	8	BH679798 BOHRS50TR
13	25	61.0	342	8	BH579888 BB579888
14	25	61.0	470	8	AQ981773 RPTC-23-3
15	25	61.0	684	8	A2615710 IM0445L01
16	25	61.0	739	9	CE636254 tigr-gss-
17	25	61.0	844	9	CR052915 Reverse s
18	24.8	60.5	683	8	CC061138 MUQO.CH25
19	24.6	60.0	658	8	BH661890 BOMT49TF
20	24.6	60.0	666	8	BZ030044 oeg01e08.
21	24.6	60.0	672	9	AG163984 Pan treg1
22	24.6	60.0	709	9	CL148048 104_327_1
23	24.6	60.0	719	9	CL148047 104_327_1
24	24.6	60.0	743	8	AZ902924 RPTC-24-1

C 25	24.4	59.5	612	2	BE436165	BE436165	EST407243
C 26	24.4	59.5	706	9	CE634961	CE634961	tigr-gss-
C 27	24.2	59.0	1225	2	AW999474	AW999474	MRO-BN07
C 28	24.2	59.0	308	2	BB605325	BB605325	BB605325
C 29	24.2	59.0	342	2	AM296976	AM296976	UI-H-BW0-
C 30	24.2	59.0	368	8	AO020044	AO020044	CIT-HSP-2
C 31	24.2	59.0	397	2	BE845728	BE845728	232923.BA
C 32	24.2	59.0	410	1	A1246601	A1246601	q65d08.x
C 33	24.2	59.0	565	4	Bj086548	Bj086548	Bj086548
C 34	24.2	59.0	613	2	BF890898	BF890898	PM2-MT010
C 35	24.2	59.0	639	5	BP147813	BP147813	BP147813
C 36	24.2	59.0	640	8	BB663865	BB663865	BB663865
C 37	24.2	59.0	688	8	BZ014247	BZ014247	ce158902
C 38	24.2	59.0	856	4	BG843226	BG843226	1024002A0
C 39	24.2	59.0	2740	3	AK086969	AK086969	Mus muscu
C 40	24	58.5	200	2	BF170224	BF170224	PCL0455.M
C 41	24	58.5	265	1	A1058636	A1058636	UI-R-C1-X
C 42	24	58.5	298	2	BF457396	BF457396	UI-M-B21-
C 43	24	58.5	308	2	CG430266	CG430266	ZMMBB025
C 44	24	58.5	310	2	AM805973	AM805973	CV1-IM010
C 45	24	58.5	313	5	BQ195494	BQ195494	UI-R-CN1-
C 46	24	58.5	392	2	AW693080	AW693080	NF050A03S
C 47	24	58.5	422	2	AW136099	AW136099	UI-H-B1-
C 48	24	58.5	479	7	H50650	H50650	yp66c02.51
C 49	24	58.5	499	5	EX083094	EX083094	EX083094
C 50	24	58.5	512	9	CG706909	CG706909	BARC.BFGL
C 51	24	58.5	570	8	AZ254746	AZ254746	1165-101
C 52	24	58.5	570	8	AZ903150	AZ903150	RPTC-24-1
C 53	24	58.5	594	5	BUS51077	BUS51077	GM880006B
C 54	24	58.5	603	2	AM044394	AM044394	wx10f09.x
C 55	24	58.5	623	9	CG035936	CG035936	PuixM11TB
C 56	24	58.5	629	6	CD402926	CD402926	Gm.CR2553
C 57	24	58.5	637	8	AO327166	AO327166	nbxb0040D
C 58	24	58.5	659	5	BK645610	BK645610	DKFZ781D
C 59	24	58.5	664	8	BZ953572	BZ953572	CH240-126
C 60	24	58.5	703	8	BZ509079	BZ509079	BONP187TR
C 61	24	58.5	714	8	BH257332	BH257332	CH230-243
C 62	24	58.5	720	8	BH280808	BH280808	CH230-97E
C 63	24	58.5	724	9	CC505950	CC505950	CH240-347
C 64	24	58.5	734	9	AC372289	AC372289	Mus.muscu
C 65	24	58.5	740	8	BH537638	BH537638	BOGV886TR
C 66	24	58.5	829	2	BF694440	BF694440	602061617
C 67	24	58.5	1041	9	CL493103	CL493103	SA11_574
C 68	24	58.5	1290	9	CL643646	CL643646	CH213-53H
C 69	24	58.0	149	9	CR497547	CR497547	Medicago
C 70	23.8	58.0	394	1	A1454568	A1454568	UI-R-BT0-
C 71	23.8	58.0	526	7	CN755384	CN755384	ID0AA15C
C 72	23.8	58.0	563	7	CO470143	CO470143	SGP170073
C 73	23.8	58.0	884	5	BU169441	BU169441	TELEACOURT
C 74	23.8	58.0	950	4	CNS0292V	CNS0292V	Teleacodon
C 75	23.8	58.0	1162	1	AV360132	AV360132	CH261-22G
C 76	23.6	57.6	262	1	AM157922	AM157922	AV360132
C 77	23.6	57.6	308	2	AM315792	AM315792	13447.MAR
C 78	23.6	57.6	322	9	CE074585	CE074585	tigr-gss-
C 79	23.6	57.6	440	4	BG511638	BG511638	sad07906
C 80	23.6	57.6	452	8	BZ856509	BZ856509	CH240-268
C 81	23.6	57.6	526	4	BM882454	BM882454	CH01h03.Y
C 82	23.6	57.6	534	8	BZ760022	BZ760022	622_1U2.C
C 83	23.6	57.6	542	8	CR294587	CR294587	Medicago
C 84	23.6	57.6	700	8	CC069234	CC069234	CSU-K33.r
C 85	23.6	57.6	763	8	AO412002	AO412002	CPG0952B
C 86	23.6	57.6	801	7	CN650171	CN650171	v6.p3_230
C 87	23.6	57.6	832	8	BZ209207	BZ209207	CH230-379
C 88	23.6	57.6	886	8	AZ202373	AZ202373	SP_0057.A
C 89	23.6	57.6	894	9	CC493317	CC493317	CH240_327
C 90	23.6	57.6	960	5	BU913485	BU913485	AGENCOURT
C 91	23.6	57.6	1201	8	CC222660	CC222660	CH261-40A
C 92	23.6	57.1	240	9	CE213483	CE213483	tigr-gss-
C 93	23.4	57.1	242	5	BO853432	BO853432	CGE20H12.
C 94	23.4	57.1	249	5	BO849247	BO849247	OGA9601.Y
C 95	23.4	57.1	276	5	BO849036	BO849036	OGA8M17.Y
C 96	23.4	57.1	317	5	BO858034	BO858034	OGB9C16.Y
C 97	23.4	57.1	328	5	BO984287	BO984287	OGGE21E10.

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OK nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 : Search time 158.775 Seconds
(without alignments)
1324.090 Million cell updates/sec

Title: US-10-035-833a-7074

Perfect score: 1 tctccatagtgtaaaaaa.....gtccacaatagtgtaaat 41

Sequence: 1 tctccatagtgtaaaaaa.....gtccacaatagtgtaaat 41

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubna/PC1_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubna/PC105_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubna/US09D_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubna/US10F_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubna/US10G_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubna/US50_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubna/US50_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	16	US-10-035-833a-7074
2	41	100.0	533	13	US-10-027-632-245152
3	41	100.0	533	13	US-10-027-632-245153
4	41	100.0	533	15	US-10-027-632-245152
5	41	100.0	533	15	US-10-027-632-245153
6	41	100.0	2181	10	US-09-999-686-10
7	41	100.0	2721	10	US-09-999-686-12
8	41	100.0	3118	10	US-09-999-686-19
9	41	100.0	3785	9	US-09-925-302-44
10	41	100.0	3785	10	US-09-925-302-44
11	41	100.0	5102	9	US-09-919-497-8
12	41	100.0	5102	9	US-09-954-531-153

13	41	100.0	5102	10	US-09-960-706-938	Sequence 918, App
14	41	100.0	5102	10	US-09-873-319-615	Sequence 615, App
15	41	100.0	5102	15	US-10-204-752-36	Sequence 16, App
16	41	100.0	5102	16	US-10-641-643-1426	Sequence 1426, App
17	41	100.0	5102	17	US-10-775-169-230	Sequence 230, App
18	41	100.0	5128	15	US-10-177-293-95	Sequence 95, App
19	41	100.0	5128	15	US-10-170-385-138	Sequence 138, App
20	41	100.0	5128	15	US-10-170-385-136	Sequence 326, App
21	41	100.0	5128	15	US-10-172-118-433	Sequence 433, App
22	41	100.0	5128	16	US-10-342-887-433	Sequence 433, App
23	41	100.0	5134	10	US-09-999-666-1	Sequence 1, App
24	41	100.0	5129	15	US-10-240-965-157	Sequence 157, App
25	29.8	72.7	630	14	US-10-198-846-7990	Sequence 7990, App
26	26.6	64.9	5371	16	US-10-221-714A-525	Sequence 525, App
27	25.6	62.4	700	13	US-10-027-632-25532	Sequence 25532, App
28	25.6	62.4	700	15	US-10-027-632-25532	Sequence 25532, App
29	24.6	60.0	60968	15	US-10-085-117-181	Sequence 181, App
30	24.2	59.0	715517	13	US-10-027-632-53712	Sequence 53712, App
31	24.2	59.0	715517	15	US-10-027-632-53712	Sequence 53712, App
32	24	58.5	50781	10	US-10-087-192-769	Sequence 769, App
33	24	58.5	335913	13	US-09-754-853A-2	Sequence 2, App
34	24	58.5	335913	10	US-09-754-853A-3	Sequence 3, App
35	23.8	58.0	2050	14	US-10-097-065-58	Sequence 58, App
36	23.8	58.0	2050	15	US-10-372-876-58	Sequence 58, App
37	23.6	57.6	440	16	US-10-424-599-42431	Sequence 4431, App
38	23.4	57.1	740	16	US-10-424-599-121713	Sequence 121713, App
39	23.2	56.6	371	16	US-10-242-535A-29134	Sequence 29134, App
40	23.2	56.6	371	16	US-10-085-783A-29134	Sequence 29134, App
41	23.2	56.6	490	13	US-10-027-632-204329	Sequence 204329, App
42	23.2	56.6	490	15	US-10-027-632-204329	Sequence 204329, App
43	23.2	56.6	207433	16	US-10-126-022-5	Sequence 5, App
44	23.2	56.6	207433	16	US-10-126-022-5	Sequence 5, App
45	23	56.1	152	16	US-10-242-535A-29614	Sequence 29614, App
46	23	56.1	152	16	US-10-085-783A-29614	Sequence 29614, App
47	23	56.1	432	16	US-10-242-535A-26442	Sequence 26442, App
48	23	56.1	432	16	US-10-085-783A-26442	Sequence 26442, App
49	23	56.1	458	13	US-10-027-632-57229	Sequence 57229, App
50	23	56.1	458	13	US-10-027-632-57230	Sequence 57230, App
51	23	56.1	458	13	US-10-027-632-309952	Sequence 309952, App
52	23	56.1	458	13	US-10-027-632-309953	Sequence 309953, App
53	23	56.1	458	15	US-10-027-632-57229	Sequence 57229, App
54	23	56.1	458	15	US-10-027-632-57230	Sequence 57230, App
55	23	56.1	458	15	US-10-027-632-309952	Sequence 309952, App
56	23	56.1	458	15	US-10-027-632-309953	Sequence 309953, App
57	23	56.1	536	13	US-10-027-632-237746	Sequence 237746, App
58	23	56.1	536	15	US-10-027-632-237746	Sequence 237746, App
59	23	56.1	605	13	US-10-027-632-319085	Sequence 319085, App
60	23	56.1	605	13	US-10-027-632-319085	Sequence 319085, App
61	23	56.1	605	15	US-10-027-632-319085	Sequence 319085, App
62	23	56.1	605	15	US-10-027-632-319085	Sequence 319085, App
63	23	56.1	748	13	US-10-027-632-24226	Sequence 24226, App
64	23	56.1	748	15	US-10-027-632-24226	Sequence 24226, App
65	23	56.1	749	13	US-10-027-632-150036	Sequence 150036, App
66	23	56.1	749	13	US-10-027-632-150036	Sequence 150036, App
67	23	56.1	902	13	US-10-027-632-4699	Sequence 4699, App
68	23	56.1	902	13	US-10-027-632-4699	Sequence 4699, App
69	23	56.1	902	15	US-10-027-632-4699	Sequence 4699, App
70	23	56.1	902	15	US-10-027-632-4699	Sequence 4699, App
71	23	56.1	2000	9	US-09-938-842A-4425	Sequence 4425, App
72	23	56.1	2000	9	US-09-938-842A-4425	Sequence 4425, App
73	23	56.1	2007	9	US-09-887-576-244	Sequence 244, App
74	23	56.1	6102	15	US-10-311-485-1472	Sequence 1472, App
75	23	56.1	50502	17	US-10-322-281-246	Sequence 246, App
76	22.8	55.6	2798	13	US-10-027-632-112257	Sequence 112257, App
77	22.8	55.6	2798	15	US-10-027-632-112257	Sequence 112257, App
78	22.8	55.6	169139	14	US-10-067-514-1	Sequence 1, App
79	22.8	55.6	169139	16	US-10-419-723-1	Sequence 1, App
80	22.6	55.1	631	13	US-10-027-632-188499	Sequence 188499, App
81	22.6	55.1	631	13	US-10-027-632-188499	Sequence 188499, App
82	22.6	55.1	748	13	US-10-027-632-27612	Sequence 27612, App
83	22.6	55.1	748	13	US-10-027-632-27612	Sequence 27612, App
84	22.6	55.1	350764	15	US-10-087-192-1864	Sequence 1864, App
85	22.6	55.1	378361	10	US-09-001-133-3	Sequence 3, App

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 : Search time 37.1814 Seconds
(without alignments)
783.789 Million cell updates/sec

Title: US-10-035-833A-7074

Perfect score: 41
Sequence: 1 tcccatagtgtaaaaaa.....gtccaccaatagtgtaaat 41

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	5102	4	US-09-023-655-1426
2	41	100.0	5102	4	US-09-919-497-8
3	22.6	55.1	930	4	US-09-220-132-89
4	22.4	54.6	273	4	US-09-621-976-11078
5	22.4	54.6	1486	1	US-08-250-859-1
6	22.4	54.6	1486	1	US-08-347-029-1
7	22.4	54.6	1486	1	US-08-490-803-1
8	22.4	54.6	1486	2	US-08-457-254-1
9	22.4	54.6	1486	2	US-08-484-257-1
10	22.4	54.6	1486	3	US-08-999-927-3
11	22.4	54.6	1486	3	US-08-461-819-3
12	22.4	54.6	1486	5	PCT-US94-08806-1
13	22.4	54.6	1486	5	PCT-US95-01775-1
14	22.4	54.6	1486	5	PCT-US95-01829-3
15	22.4	54.6	1486	5	PCT-US95-14932-1
16	22.4	54.6	1486	5	PCT-US95-16626-1
17	22.2	54.1	168575	4	US-09-426-280-1
18	22.2	54.1	480	4	US-09-270-767-30573
19	22.2	53.7	572	4	US-09-270-767-14411
20	21.8	53.2	2621	4	US-09-673-335A-22
21	21.6	52.7	540	4	US-09-248-796A-6021
22	21.4	52.2	1863	4	US-09-248-796A-2811
23	21.4	52.2	99629	4	US-09-596-002-37
24	21.2	51.7	6400	4	US-09-976-594-61
25	21.2	51.7	193	4	US-09-513-989C-24677
26	21.2	51.2	265	4	US-09-513-989C-36085
27	21.2	51.2	970	3	US-08-791-115B-16

28	21	51.2	970	4	US-09-140-749-27	Sequence 27, Appl
29	21	51.2	3680	4	US-09-647-390-15	Sequence 15, Appl
30	21	51.2	4084	2	US-08-568-459A-1	Sequence 1, Appl
31	21	51.2	4084	2	US-08-487-826B-1	Sequence 1, Appl
32	21	51.2	4084	3	US-09-210-288-1	Sequence 1, Appl
33	21	51.2	4084	6	5198347-5	Patent No. 5198347
34	20.8	50.7	419	4	US-09-513-999C-31472	Sequence 31472, A
35	20.8	50.7	471	4	US-09-270-767-5979	Sequence 5979, Ap
36	20.8	50.7	471	4	US-09-270-767-1261	Sequence 1261, A
37	20.8	50.7	599	4	US-09-270-767-12759	Sequence 12759, A
38	20.8	50.7	1419	4	US-09-270-767-10657	Sequence 10657, A
39	20.8	50.7	1665	4	US-09-614-221A-65	Sequence 65, Appl
40	20.8	50.7	2594	4	US-10-140-002-145	Sequence 245, Appl
41	20.8	50.7	2940	4	US-09-248-796A-5139	Sequence 5139, Ap
42	20.8	50.7	3585	4	US-09-270-767-14479	Sequence 14479, A
43	20.8	50.7	4825	6	5459251-1	Patent No. 5459251
44	20.8	50.7	5086	2	US-08-465-485A-19	Sequence 19, Appl
45	20.8	50.7	5086	2	US-08-365-486A-14	Sequence 14, Appl
46	20.8	50.7	5086	3	US-09-080-285-19	Sequence 19, Appl
47	20.8	50.7	5086	3	US-08-880-342-14	Sequence 14, Appl
48	20.8	50.7	5086	4	US-09-724-426-19	Sequence 19, Appl
49	20.8	50.7	5086	4	US-09-233-527-7	Sequence 7, Appl
50	20.8	50.7	5086	5	PCT-US93-06651-4	Sequence 4, Appl
51	20.8	50.7	5086	5	PCT-US93-06651-2	Sequence 2, Appl
52	20.8	50.7	5094	3	US-08-224-186-7	Sequence 7, Appl
53	20.8	50.7	5104	6	5506344-1	Patent No. 5506344
54	20.8	50.7	1656	4	US-09-433-579-3	Sequence 3, Appl
55	20.8	50.7	38844	3	US-09-734-675-3	Sequence 3, Appl
56	20.8	50.7	148567	4	US-09-801-876B-3	Sequence 3, Appl
57	20.8	50.7	148567	4	US-10-254-869-3	Sequence 3, Appl
58	20.8	50.7	580073	4	US-08-545-528D-1	Sequence 1, Appl
59	20.8	50.7	1654976	4	US-08-916-421B-1	Sequence 1, Appl
60	20.8	50.7	1654976	4	US-09-692-570-1	Sequence 1, Appl
61	20.6	50.2	237	4	US-09-248-796A-7725	Sequence 7725, Ap
62	20.6	50.2	414	4	US-09-513-999C-9073	Sequence 9073, Ap
63	20.6	50.2	242	4	US-09-248-796A-5571	Sequence 5571, Ap
64	20.6	50.2	1569	2	US-08-743-637B-176	Sequence 176, App
65	20.6	50.2	1569	3	US-08-526-480B-176	Sequence 176, App
66	20.6	50.2	4612	4	US-09-023-655-956	Sequence 956, App
67	20.6	50.2	1230028	4	US-09-198-452A-1	Sequence 1, Appl
68	20.6	50.2	1664976	4	US-08-916-421B-1	Sequence 1, Appl
69	20.6	50.2	1664976	4	US-09-692-570-1	Sequence 1, Appl
70	20.4	49.8	201	4	US-09-248-796A-13699	Sequence 13699, A
71	20.4	49.8	665	3	US-09-030-607-196	Sequence 196, App
72	20.4	49.8	665	3	US-09-439-313-196	Sequence 196, App
73	20.4	49.8	665	3	US-09-352-616A-196	Sequence 196, App
74	20.4	49.8	665	4	US-09-232-149A-196	Sequence 196, App
75	20.4	49.8	665	4	US-09-159-812-196	Sequence 196, App
76	20.4	49.8	665	4	US-09-636-215-196	Sequence 196, App
77	20.4	49.8	665	4	US-09-685-166A-196	Sequence 196, App
78	20.4	49.8	665	4	US-09-115-453-196	Sequence 196, App
79	20.4	49.8	665	4	US-09-688-489-196	Sequence 196, App
80	20.4	49.8	665	4	US-09-679-426-196	Sequence 196, App
81	20.4	49.8	979	4	US-09-786-480B-6	Sequence 6, Appl
82	20.4	49.8	1065	4	US-09-546-986A-7	Sequence 7, Appl
83	20.4	49.8	1065	4	US-09-524-730-7	Sequence 7, Appl
84	20.4	49.8	1135	3	US-08-936-165A-135	Sequence 135, App
85	20.4	49.8	2517	4	US-09-857-556A-11	Sequence 11, Appl
86	20.4	49.8	4406	1	US-08-369-043-1	Sequence 1, Appl
87	20.4	49.8	5152	4	US-10-204-708-48	Sequence 48, Appl
88	20.4	49.8	64467	4	US-09-801-671B-3	Sequence 32, Appl
89	20.4	49.8	118999	4	US-09-791-105B-32	Sequence 32, Appl
90	20.4	49.8	202001	4	US-09-734-674-3	Sequence 3, Appl
91	20.4	49.8	1830121	4	US-09-557-884-1	Sequence 1, Appl
92	20.4	49.8	1830121	4	US-09-643-990A-1	Sequence 1, Appl
93	20.4	49.8	1830121	4	US-10-139-960-1	Sequence 1, Appl
94	20.2	49.3	207	4	US-09-270-767-30830	Sequence 30830, A
95	20.2	49.3	973	4	US-09-270-767-2044	Sequence 2044, App
96	20.2	49.3	973	4	US-09-270-767-15486	Sequence 15486, A
97	20.2	49.3	991	4	US-09-270-767-14621	Sequence 14621, A
98	20.2	49.3	1059	4	US-09-248-796A-1305	Sequence 1305, App
99	20.2	49.3	1266	3	US-09-134-078-3	Sequence 3, Appl
100	20.2	49.3	1662	4	US-09-134-000C-666	Sequence 666, App

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 Seconds
(without alignments)
1214.152 Million cell updates/sec

Title: US-10-035-833A-7074

Perfect score: 1 tctcatagcttaaaaaaaaa.....gtccaccaatagtcgaaat 41

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
1: Geneseq_23Sep04:*
2: Geneseq_1980s:*
3: Geneseq_1990s:*
4: Geneseq_2000s:*
5: Geneseq_2001as:*
6: Geneseq_2001bs:*
7: Geneseq_2002as:*
8: Geneseq_2002bs:*
9: Geneseq_2003as:*
10: Geneseq_2003cs:*
11: Geneseq_2003ds:*
12: Geneseq_2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	41	100.0	41	6	Abz50292 Human CYC
2	41	100.0	3785	3	AAFI8025 Lung can
3	41	100.0	5102	6	ABQ79929 Human CYP
4	41	100.0	5102	6	ABK35488 Human end
5	41	100.0	5102	6	ABL62883 Breast ca
6	41	100.0	5102	6	ABK64720 Human ben
7	41	100.0	5102	6	AAI39861 Human all
8	41	100.0	5102	10	ADP14611 Human strc
9	41	100.0	5102	10	ACG46768 Human COP
10	41	100.0	5102	11	AD132100 Human CDN
11	41	100.0	5128	6	ABV78036 Hypoxia-r
12	41	100.0	5128	6	ABV77942 Hypoxia-r
13	41	100.0	5128	6	ACF34492 Gene enco
14	41	100.0	5128	8	ACC50124 Breast ca
15	41	100.0	5128	12	ADN03862 Antipscor
16	41	100.0	5134	6	ABK88882 Human CYP
17	41	100.0	5329	6	AA594902 Human DNA
18	41	100.0	10254	6	ABN81206 Human CYP
19	29.8	72.7	297	4	AAI25712 Human bre
20	29.8	72.7	307	4	AAI26762 Human bre
21	29.8	72.7	311	4	AAI18107 Human bre

22	29.8	72.7	365	4	AAI07966 Human bre
23	26.6	64.9	5371	4	AA546799 Tumour su
24	58.5	3355	10	AD64106 Human gen	
25	58.5	3355	10	AD64110 Human gen	
26	58.5	335913	5	AAI61371 Soybean 2	
27	58.5	335913	5	AAI61372 Soybean 2	
28	58.0	2050	2	AAK97997 Human sec	
29	58.0	2050	9	ADAI1530 Human CDN	
30	56.6	11481	4	AAK71590 Human imm	
31	56.6	57038	11	ADPE5343 Human seq	
32	56.6	80578	4	AAH44800 Human GPC	
33	56.6	81369	3	AAK97997 Human T g	
34	56.6	92794	11	ADPE5471 Human seq	
35	56.6	207433	5	ABZ72040 Gene 216	
36	56.6	207433	8	ABK74891 BAC10812	
37	56.6	207433	12	ADJ36614 Bacterial	
38	56.6	207433	12	ADJ61193 BAC10982	
39	56.1	2000	6	ABZ16620 Arabidops	
40	56.1	3014	4	AAK81019 Human imm	
41	56.1	3014	4	AAK82052 Human imm	
42	56.1	6102	6	ABL35499 Human imm	
43	56.1	25003	4	AAK82053 Human imm	
44	56.1	25003	4	AAK81020 Human imm	
45	55.6	110000	6	ABX08336_01 Continuation (2 of	
46	55.6	110000	12	ADJ25985_01 Continuation (2 of	
47	55.6	110000	12	ADN87989_01 Continuation (2 of	
48	55.6	110000	12	ADOS0281_01 Continuation (2 of	
49	55.1	930	10	ADB13173 Testosterone	
50	55.1	110000	10	Continuation (2 of	
51	55.1	192427	10	ADL13825 Osteoarthritis	
52	55.1	192427	10	ADP72091 Renal toxicology	
53	54.6	316	12	ACH67795 Human genome	
54	54.6	530	12	AAQ94110 MML2 gene	
55	54.6	1443	2	AAQ94111 MML2 gene	
56	54.6	1486	2	AAAT03942 Mouse thymus	
57	54.6	1486	2	AAAT04045 Sequence	
58	54.6	1486	2	AAQ97690 Haematopoiesis	
59	54.6	1486	2	AAAT37382 Mouse thymus	
60	54.6	1486	2	AAAT34851 Mouse thymus	
61	54.6	1486	2	AAAT32590 Mouse thymus	
62	54.6	1486	3	AAZ37784 Mouse thymus	
63	54.6	1486	3	AAAS1992 Murine thymus	
64	54.6	1536	2	AAQ94111 MML2 gene	
65	54.6	1743	12	ADM66956 Human adipose	
66	54.6	1765	4	AAH57384 Human skin	
67	54.6	2000	6	ABZ16938 Arabidopsis	
68	54.6	2000	8	ADA68938 Arabidopsis	
69	54.6	2037	8	ACA29508 Prokaryote	
70	54.6	2094	8	ABX34690 Human rDNA	
71	54.6	2190	3	AAZ51263 Human RNA	
72	54.6	2286	6	ABQ93392 Human cDNA	
73	54.6	2286	12	ADQ22835 Human soft tissue	
74	54.6	5425	6	ABL19311 Mouse islet	
75	54.6	6078	6	ABL13345 Human immunoglobulin	
76	54.6	7857	6	ABQ67076 Human angiogenesis	
77	54.6	10480	6	AAZ51263 Human RNA	
78	54.6	10480	8	AAZ51263 Human RNA	
79	54.6	110000	10	ADCE1169_2 Continuation (5 of	
80	54.6	222880	10	ADCE1169_2 Continuation (3 of	
81	54.1	488	4	AA78591 Plant SDF	
82	54.1	1427	4	AA532397 Human cDNA	
83	54.1	1427	4	AA532810 Human gene	
84	54.1	3679	4	AAZ12508 Human gene	
85	54.1	10250	6	ABN80083 Human chitinase	
86	54.1	15188	4	ABL25090 Human hypoxanthine	
87	54.1	168575	4	AAH21613 Human hypoxanthine	
88	54.1	198285	6	ABK84699 Human cDNA	
89	54.1	198285	6	ABN97319 Gene #381	
90	54.1	260209	6	AB556564 Human SUT	
91	54.1	260209	12	ADN16204 Human SUT	
92	53.7	1003	12	ADQ25325 Human soft tissue	
93	53.7	1301	12	ADQ25325 Human soft tissue	
94	53.7	1690	5	AA578453 DNA encoding	
95	53.7	1690	5	AA578453 DNA encoding	

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 : Search time 720.113 Seconds
(without alignments)
2692.464 Million cell updates/sec

Title: US-10-035-833a-7074
Perfect score: 41
Sequence: 1 tctcataggtctaaaaaa.....gtcccaaatagtgtaaat 41

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: GenEmbl:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

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8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	2181	6	AX666080 Sequence
2	41	100.0	2721	6	AX666082 Sequence
3	41	100.0	3118	6	AX666089 Sequence
4	41	100.0	5102	6	BD176699 Method of
5	41	100.0	5102	6	AR380881 Sequence
6	41	100.0	5102	6	AX330711 Sequence
7	41	100.0	5102	6	AX663644 Sequence
8	41	100.0	5102	6	BD169898 Method of
9	41	100.0	5102	6	HSU03688 Human dioxi
10	41	100.0	5104	6	CO714214 Sequence
11	41	100.0	5134	6	AX666071 Sequence
12	41	100.0	5234	11	BY177879 seqm97309
13	41	100.0	5329	6	AX281748 Sequence
14	41	100.0	12124	9	AY393998 Homo sapi
15	41	100.0	12177	9	HSU56438 Human dioxi
16	41	100.0	79303	2	AC011074 Homo sapi
17	41	100.0	209156	2	AC009229 Homo sapi
18	41	100.0	211222	2	AC022097 Homo sapi
19	40	97.6	41	6	AX520876 Sequence

20	31	75.6	3124	11	G06772
21	29.8	72.7	297	6	CQ433148
22	29.8	72.7	307	6	CQ434199
23	29.8	72.7	311	6	CQ425540
24	29.8	72.7	365	6	CQ415389
25	27.8	67.8	65118	9	AC084187
26	27.8	67.8	11682	9	AL672277
27	26.8	65.4	173525	2	AC067893
28	26.8	65.4	184585	2	AC079465
29	26.8	65.4	184649	2	AC025185
30	26.6	64.9	5371	6	AX251557
31	26.6	64.9	149442	10	AC116180
32	26.6	64.9	169768	10	AC147631
33	26.6	64.9	173198	9	AC108132
34	26.2	63.9	157775	8	AC102331
35	26.2	63.9	161741	8	AC120535
36	26.2	63.9	170020	8	AC138001
37	25.8	62.9	5830	8	AY158836
38	25.8	62.9	139280	8	AC099052
39	25.8	62.9	171461	9	AC097041
40	25.8	62.9	185161	9	AC006059
41	25.8	62.9	194742	9	AC092047
42	25.6	62.4	128074	8	AC145165
43	25.6	62.4	143254	5	BX649263
44	25.6	62.4	145342	2	AC023220
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46	25.6	62.4	161790	2	AC023371
47	25.6	62.4	169327	5	BX957258
48	25.6	62.4	201088	9	AL585733
49	25.6	62.4	205013	2	AC128805
50	25.6	62.4	228377	2	BX897723
51	25.6	62.4	230856	2	AC133817
52	25.6	62.4	234077	2	AC130857
53	25.6	62.4	259063	2	AC113390
54	25.4	62.0	197911	10	AL805957
55	25.4	62.0	223873	2	AC107198
56	25.4	62.0	224436	2	AC107405
57	25.4	62.0	231404	2	AC127772
58	25.4	62.0	233342	2	AC096410
59	25.4	62.0	238565	2	AC096802
60	25.2	61.5	337	11	G12267
61	25.2	61.5	114707	2	AC146332
62	25.2	61.5	132745	2	AC068647
63	25.2	61.5	139435	2	AC068635
64	25.2	61.5	140556	2	AC078807
65	25	61.0	97734	9	AC095066
66	25	61.0	127148	2	AP002081
67	25	61.0	145246	10	AC115906
68	25	61.0	147519	2	AC079099
69	25	61.0	155584	5	BX294385
70	25	61.0	164271	2	AC009571
71	25	61.0	169604	2	BX640595
72	25	61.0	175131	10	AC127681
73	25	61.0	181230	5	BX296556
74	25	61.0	191961	2	AC111828
75	25	61.0	217266	10	AC124177
76	25	61.0	222162	10	AC109281
77	25	61.0	225655	10	AC099690
78	25	61.0	245784	10	AC099863
79	25	61.0	279425	2	AC128006
80	24.8	60.5	52000	2	AC146829
81	24.8	60.5	165098	2	AC146832
82	24.8	60.5	183543	10	AL670360
83	24.8	60.5	187604	2	AC136384
84	24.8	60.5	201262	2	AC118512
85	24.8	60.5	203300	9	AC008744
86	24.8	60.5	218882	2	AC148459
87	24.6	60.0	339503	2	AC101063
88	24.6	60.0	134608	2	AC146839
89	24.6	60.0	137475	5	BX005277
90	24.6	60.0	174866	5	BX510916
91	24.6	60.0	182715	2	AC130031
92	24.6	60.0	183068	2	CR354422

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CQ425540	Sequence		
CQ415389	Sequence		
AC084187	Homo sapi		
AL672277	Human DNA		
AC067893	Homo sapi		
AC079465	Homo sapi		
AC025185	Homo sapi		
AX251557	Sequence		
AC116180	Mus muscu		
AC147631	Mus muscu		
AC108132	Mus muscu		
AC102331	Mus muscu		
AC120535	Oryza sat		
AC138001	Oryza sat		
AY158836	Fraxaria		
AC099052	Homo sapi		
AC097041	Homo sapi		
AC006059	Homo sapi		
AC092047	Homo sapi		
AC145165	Medicago		
BX649263	Zebrafish		
AC023220	Homo sapi		
AC023220	Homo sapi		
AC023371	Homo sapi		
BX957258	Zebrafish		
AL585733	Human DNA		
AC128805	Rattus no		
BX897723	Danio rer		
AC133817	Rattus no		
AC130857	Rattus no		
AC113390	Rattus no		
AL805957	Mouse DNA		
AC107198	Rattus no		
AC107405	Rattus no		
AC127772	Rattus no		
AC096410	Rattus no		
AC096802	Rattus no		
G12267	UNH114 Tila		
AC146332	Medicago		
AC068647	Homo sapi		
AC068635	Homo sapi		
AC078807	Homo sapi		
AC095066	Homo sapi		
AP002081	Homo sapi		
AC115906	Mus muscu		
AC079099	Homo sapi		
BX294385	Zebrafish		
AC009571	Homo sapi		
BX640595	Danio rer		
AC127681	Mus muscu		
BX296556	Zebrafish		
AC111828	Rattus no		
AC124177	Mus muscu		
AC109281	Mus muscu		
AC099690	Mus muscu		
AC099863	Mus muscu		
AC128006	Rattus no		
AC146829	Mus muscu		
AC146832	Mus muscu		
AL670360	Mouse DNA		
AC136384	Rattus no		
AC118512	Rattus no		
AC008744	Xenopus t		
AC148459	Mus muscu		
AC101063	Mus muscu		
AC146839	Dasytus n		
BX005277	Zebrafish		
BX510916	Zebrafish		
AC130031	Rattus no		
CR354422	Danio rer		

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 : Search time 1452.89 Seconds
(without alignments)
1028.317 Million cell updates/sec

Title: US-10-035-833A-7073

Perfect score: 41
Sequence: 1 tcagcaagaataaaaaa.....gccagccaagcttaacta 41

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	36	87.8	201	7	W03094
4	32.8	80.0	663	5	BU686928 UI-CF-D01
5	31.8	77.6	339	2	BE925815 QV0-BN004
6	30.2	73.7	225	2	AW999474 MRO-BN007
7	29.4	71.7	409	6	CD698653 EST15176
8	28	68.3	1004	4	BI522407 603081321
9	27.4	66.8	374	7	CF431938 NIT1.16.H
10	27.4	66.8	565	7	CN682584 E0166G06-
11	27.4	66.8	815	5	BX689954 BX689954
12	27.2	66.3	621	8	AQ373552 RPCI1.1-15
13	27.2	66.3	745	4	BG531495 602561679
14	27.2	66.3	881	8	AZ753829 RPCI-24-1
15	27.2	66.3	1131	8	C2208497 C2261-111
16	27	65.9	550	9	CE177608 t1gr-g88-
17	27	65.9	823	5	BU218198 603105762
18	27	65.9	845	8	CC389109 PHB866TD
19	27	65.9	906	9	CL117859 ISB1-69F2
20	26.8	65.4	286	1	AA185458 mu47a08.r
21	26.8	65.4	447	5	BY541727
22	26.8	65.4	477	1	AA597168 v024a09.r
23	26.8	65.4	635	5	BQ206621 UI-R-D21-
24	26.8	65.4	687	9	CC957683 BO1BD677R

C	25	26.8	65.4	690	7	CN438494
C	26	26.8	65.4	782	9	AG439136 Mus_muscu
C	27	26.6	64.9	610	5	BX694247 BX694247
C	28	26.6	64.9	729	9	CR077759 Reverse.s
C	29	26.6	64.9	774	7	CR427047
C	30	26.6	64.9	807	5	BX687032 BX687032
C	31	26.6	64.9	808	5	BX701131 BX701131
C	32	26.6	64.9	809	5	BX686008 BX686008
C	33	26.6	64.9	811	5	CC522028 CC522028
C	34	26.6	64.9	814	5	BX693986 BX693986
C	35	26.4	64.4	588	8	AZ996084 AZ996084
C	36	26.4	64.4	753	9	CC560820 CC560820
C	37	26.4	64.4	958	5	BQ723128 BQ723128
C	38	26.4	64.4	1200	3	CR698500 CR698500
C	39	26.2	63.9	137	6	CB913091 CB913091
C	40	26.2	63.9	182	9	CG790081 CG790081
C	41	26.2	63.9	466	8	AZ345022 AZ345022
C	42	26.2	63.9	506	9	CG977564 CG977564
C	43	26.2	63.9	648	6	CD714444 CD714444
C	44	26.2	63.9	733	9	CL795859 CL795859
C	45	26.2	63.9	929	9	CNS051KY CNS051KY
C	46	26.2	63.4	180	1	AV065791 AV065791
C	47	26	63.4	437	7	CF897830 CF897830
C	48	26	63.4	443	2	AW763630 AW763630
C	49	26	63.4	493	1	AI020196 AI020196
C	50	26	63.4	543	8	BH859469 BH859469
C	51	26	63.4	548	4	BG144175 BG144175
C	52	26	63.4	605	8	AZ842743 AZ842743
C	53	26	63.4	642	2	BE336468 BE336468
C	54	26	63.4	694	5	BP149851 BP149851
C	55	26	63.4	785	7	CK031740 CK031740
C	56	26	63.4	833	5	BU362978 BU362978
C	57	26	63.4	882	6	CA470932 CA470932
C	58	26	63.4	1027	5	BG519054 BG519054
C	59	26	63.4	1143	5	AX463464 AX463464
C	60	26	63.4	238	5	BY545680 BY545680
C	61	26	63.4	288	5	BY530462 BY530462
C	62	26	63.4	390	5	BX615697 BX615697
C	63	26	63.4	443	2	AW532503 AW532503
C	64	26	63.4	551	6	CA917438 CA917438
C	65	26	63.4	560	4	BG451579 BG451579
C	66	26	63.4	582	8	AZ314547 AZ314547
C	67	26	63.4	594	8	AZ961610 AZ961610
C	68	26	63.4	941	6	CD795914 CD795914
C	69	26	63.4	1037	7	CNS01780 CNS01780
C	70	26	63.4	349	7	CK727545 CK727545
C	71	26	63.4	364	1	AA233852 AA233852
C	72	26	63.4	410	4	EM033337 EM033337
C	73	26	63.4	417	1	AJ688430 AJ688430
C	74	26	63.4	424	1	CB796172 CB796172
C	75	26	63.4	466	1	AI694480 AI694480
C	76	26	63.4	498	4	BM254648 BM254648
C	77	26	63.4	499	7	CE727174 CE727174
C	78	26	63.4	515	5	BY365254 BY365254
C	79	26	63.4	534	8	BH457700 BQ206621
C	80	26	63.4	554	2	BF224042 BF224042
C	81	26	63.4	555	8	AO414660 AO414660
C	82	26	63.4	599	5	BX470609 BX470609

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 ; Search time 158.775 Seconds
(without alignments)
1324.090 Million cell updates/sec

Title: US-10-035-833a-7073

Perfect score: 41
Sequence: 1 tcagcaagaagaaaaaa.....gcacgcaagcttaatra 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications: NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	41	16	US-10-035-833a-7073
2	41	100.0	533	13	US-10-027-632-245152
3	41	100.0	533	13	US-10-027-632-245152
4	41	100.0	533	15	US-10-027-632-245152
5	41	100.0	533	15	US-10-027-632-245152
6	41	100.0	2181	10	US-09-999-686-10
7	41	100.0	2721	10	US-09-999-686-12
8	41	100.0	3118	10	US-09-999-686-19
9	41	100.0	5102	9	US-09-919-497-8
10	41	100.0	5102	9	US-09-954-531-153
11	41	100.0	5102	10	US-09-960-706-938
12	41	100.0	5102	10	US-09-873-319-615

13	41	100.0	5102	15	US-10-204-752-36	Sequence 36, Appl
14	41	100.0	5102	16	US-10-641-643-1426	Sequence 1426, Ap
15	41	100.0	5102	17	US-10-775-169-230	Sequence 230, App
16	41	100.0	5128	15	US-10-177-293-95	Sequence 95, Appl
17	41	100.0	5128	15	US-10-170-385-136	Sequence 136, App
18	41	100.0	5128	15	US-10-170-385-326	Sequence 326, App
19	41	100.0	5128	15	US-10-172-118-433	Sequence 433, App
20	41	100.0	5128	16	US-10-342-887-433	Sequence 433, App
21	41	100.0	5134	10	US-09-999-686-1	Sequence 1, Appl
22	41	100.0	5329	15	US-10-240-965-157	Sequence 157, App
23	40.6	99.0	3785	9	US-09-925-302-44	Sequence 44, Appl
24	40.6	99.0	3785	10	US-09-925-302-44	Sequence 44, Appl
25	36.2	88.3	23415	16	US-10-052-482-49	Sequence 18261, A
26	27.6	67.3	83450	10	US-10-052-482-49	Sequence 49, Appl
27	27	65.9	83450	10	US-09-811-469-3	Sequence 3, Appl
28	26.5	64.9	15832	15	US-10-239-676-105	Sequence 105, App
29	26.5	64.9	15832	15	US-10-240-453-135	Sequence 135, Ap
30	26.5	64.9	15832	15	US-10-240-453-135	Sequence 117, App
31	26.6	63.4	554	13	US-10-027-632-288971	Sequence 288971, A
32	26.6	63.4	554	13	US-10-027-632-288971	Sequence 288971, A
33	26	63.4	9261	16	US-10-052-482-50	Sequence 50, Appl
34	26	63.4	9261	16	US-10-052-482-50	Sequence 50, Appl
35	25.6	62.4	183999	17	US-10-745-377-1	Sequence 1, Appl
36	25.6	62.4	357652	17	US-10-322-696-34	Sequence 34, Appl
37	25.4	62.0	413	10	US-09-918-995-1253	Sequence 1253, A
38	25.4	62.0	2176	17	US-10-424-599-23531	Sequence 23531, A
39	25.4	62.0	165156	17	US-10-424-599-23531	Sequence 5668, Ap
40	25.2	61.5	178	16	US-10-741-601-5668	Sequence 11631, A
41	25	61.0	683	16	US-10-424-599-74570	Sequence 74570, A
42	25	61.0	761	16	US-10-425-114-12846	Sequence 12846, A
43	25	61.0	825	16	US-10-425-114-10598	Sequence 10598, A
44	25	61.0	1101	16	US-10-424-599-74567	Sequence 74567, A
45	25	61.0	3759	17	US-10-337-963-63121	Sequence 63121, A
46	25	61.0	40955	11	US-09-897-722-136	Sequence 136, App
47	25	61.0	98686	16	US-10-189-467-20	Sequence 20, Appl
48	25	61.0	153330	13	US-10-087-192-1834	Sequence 1834, App
49	24.8	60.5	427	11	US-09-864-408A-6247	Sequence 6247, Ap
50	24.8	60.5	497	10	US-09-918-995-15859	Sequence 15859, A
51	24.8	60.5	497	16	US-10-242-535A-43684	Sequence 43684, A
52	24.8	60.5	497	16	US-10-085-783A-43684	Sequence 43684, A
53	24.8	60.5	598	13	US-10-027-632-269156	Sequence 269156, A
54	24.8	60.5	598	13	US-10-027-632-269157	Sequence 269157, A
55	24.8	60.5	598	15	US-10-027-632-269156	Sequence 269156, A
56	24.8	60.5	598	15	US-10-027-632-269157	Sequence 269157, A
57	24.8	60.5	3030	13	US-10-027-632-114287	Sequence 114287, A
58	24.8	60.5	3030	13	US-10-027-632-114288	Sequence 114288, A
59	24.8	60.5	3030	15	US-10-027-632-114287	Sequence 114287, A
60	24.8	60.5	3030	15	US-10-027-632-114288	Sequence 114288, A
61	24.8	60.5	69652	17	US-10-322-281-72	Sequence 72, Appl
62	24.6	60.0	392	9	US-09-983-965-4284	Sequence 4284, Ap
63	24.6	60.0	549	16	US-10-424-599-47467	Sequence 47467, A
64	24.6	60.0	559	16	US-10-424-599-47467	Sequence 47467, A
65	24.6	60.0	889	13	US-10-027-632-172535	Sequence 172535, A
66	24.6	60.0	889	13	US-10-027-632-172536	Sequence 172536, A
67	24.6	60.0	889	15	US-10-027-632-172535	Sequence 172535, A
68	24.6	60.0	889	15	US-10-027-632-172536	Sequence 172536, A
69	24.6	60.0	5081	15	US-10-128-714-156	Sequence 156, App
70	24.6	60.0	5311	15	US-10-128-714-156	Sequence 156, App
71	24.6	60.0	1000	15	US-10-633-843-10	Sequence 10, Appl
72	24.6	60.0	41966	16	US-10-087-192-1804	Sequence 1804, Ap
73	24.6	60.0	45364	17	US-10-332-811-235	Sequence 235, App
74	24.4	59.5	500	15	US-10-029-386-7906	Sequence 7906, App
75	24.4	59.5	539	13	US-10-027-632-4931	Sequence 4931, Ap
76	24.4	59.5	539	13	US-10-027-632-4931	Sequence 4931, Ap
77	24.4	59.5	540	13	US-10-027-632-189917	Sequence 189917, A
78	24.4	59.5	540	13	US-10-027-632-189917	Sequence 189917, A
79	24.4	59.5	540	13	US-10-027-632-189917	Sequence 189917, A
80	24.4	59.5	540	13	US-10-027-632-189917	Sequence 189917, A
81	24.4	59.5	540	13	US-10-027-632-189917	Sequence 189917, A
82	24.4	59.5	1119	16	US-10-282-122A-22973	Sequence 22973, A
83	24.4	59.5	180227	17	US-10-332-281-308	Sequence 308, App
84	24.2	59.0	457	14	US-10-060-036-1577	Sequence 1577, Ap
85	24.2	59.0	481	16	US-10-424-599-114135	Sequence 114135, A

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 ; Search time 37.184 Seconds
(without alignments)
783.789 Million cell updates/sec

Title: US-10-035-833a-7073

Perfect score: 41 tcagcaagaagaaaaaa.....gccagcagcttaatra 41

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seg:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seg:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seg:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seg:*
5: /cgn2_6/ptodata/1/ina/PCPUS.COMB.seg:*
6: /cgn2_6/ptodata/1/ina/backfile1.seg:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	5102	4	US-09-023-655-1426
2	41	100.0	5102	4	US-09-919-497-8
3	27	65.9	83450	4	US-09-811-469-3
4	27	65.9	83450	4	US-10-370-659-3
5	24	58.5	1426	4	US-09-023-655-375
6	23	58.0	894	4	US-09-134-000C-211
7	23	57.1	195	4	US-09-621-976-14748
8	23	57.1	567	4	US-09-543-681A-622
9	23	57.1	645	4	US-09-385-982-40
10	23	56.6	445	4	US-09-270-767-4909
11	23	56.6	445	4	US-09-270-767-20191
12	23	56.6	2182	3	US-09-039-046-3
13	23	56.6	5666	4	US-10-204-708-30
14	23	56.1	328	4	US-09-621-976-13643
15	23	56.1	396	4	US-09-513-999C-12076
16	23	56.1	1089	4	US-09-248-796A-461
17	23	56.1	8705	4	US-09-544-398B-10
18	23	56.1	8705	4	US-09-543-771-10
19	23	56.1	9347	4	US-10-204-708-36
20	23	56.1	786431	4	US-09-751-389-3
21	22	55.6	469	4	US-09-134-000C-3073
22	22	55.6	469	4	US-09-270-767-14304
23	22	55.6	601	3	US-09-814-951A-14
24	22	55.6	1187	4	US-09-962-665-7
25	22	55.6	1187	4	US-09-663-333-7
26	22	55.6	1187	4	US-09-962-677-7
27	22	55.6	9704	3	US-09-814-951A-3

28	22.8	55.6	18596	3	US-09-318-448-11	Sequence 11, Appli
29	22.8	55.6	18597	4	US-09-962-665-8	Sequence 8, Appli
30	22.8	55.6	18597	4	US-09-963-333-8	Sequence 8, Appli
31	22.8	55.6	18597	4	US-09-962-677-8	Sequence 8, Appli
32	22.6	55.1	547	2	US-08-131-365B-41	Sequence 41, Appli
33	22.6	55.1	1801	1	US-08-668-123-41	Sequence 41, Appli
34	22.6	55.1	1801	1	US-08-557-917A-1	Sequence 1, Appli
35	22.6	55.1	1801	3	US-09-084-153-1	Sequence 1, Appli
36	22.6	55.1	1801	3	US-09-084-079-1	Sequence 1, Appli
37	22.6	55.1	4698	1	US-07-807-043B-5	Sequence 5, Appli
38	22.6	55.1	4698	1	US-08-299-849B-5	Sequence 5, Appli
39	22.6	55.1	4698	2	US-08-142-368A-5	Sequence 5, Appli
40	22.6	55.1	4698	3	US-08-967-727-5	Sequence 5, Appli
41	22.6	55.1	4698	3	US-08-037-310D-5	Sequence 5, Appli
42	22.6	55.1	4698	4	US-09-583-850-5	Sequence 5, Appli
43	22.6	55.1	4698	4	US-09-379-197-5	Sequence 5, Appli
44	22.6	55.1	4698	4	US-09-404-026-5	Sequence 5, Appli
45	22.6	55.1	4698	4	US-09-312-464-5	Sequence 5, Appli
46	22.6	55.1	54945	4	US-09-620-312D-255	Sequence 255, Appl
47	22.6	55.1	6470	4	US-09-967-669-10	Sequence 10, Appli
48	22.4	54.6	214	4	US-09-513-999C-34142	Sequence 688, Ap
49	22.4	54.6	486	4	US-09-270-767-4988	Sequence 22270, A
50	22.4	54.6	486	4	US-09-270-767-22270	Sequence 2760, Ap
51	22.4	54.6	648	4	US-09-134-000C-2760	Sequence 16, Appli
52	22.4	54.6	775	4	US-09-780-717-16	Sequence 10658, A
53	22.4	54.6	942	4	US-09-270-767-10658	Sequence 19, Appli
54	22.4	54.6	959	4	US-09-205-258-19	Sequence 7, Appli
55	22.4	54.6	1674	1	US-07-778-890-7	Sequence 7, Appli
56	22.4	54.6	1674	1	US-07-778-890-7	Sequence 7, Appli
57	22.4	54.6	1674	5	PCT-US93-05640-7	Sequence 7, Appli
58	22.4	54.6	148567	4	US-09-801-876B-3	Sequence 3, Appli
59	22.4	54.6	148567	4	US-10-254-869-3	Sequence 3, Appli
60	22.2	54.1	55298	4	US-09-491-356C-1	Sequence 1, Appli
61	22.2	54.1	193303	4	US-09-497-855A-37	Sequence 37, Appli
62	22.2	54.1	193303	4	US-09-497-855A-44	Sequence 44, Appli
63	22	53.7	39	4	US-09-632-313A-6	Sequence 6, Appli
64	22	53.7	39	4	US-09-921-942B-5	Sequence 5, Appli
65	22	53.7	117	4	US-09-404-879A-359	Sequence 359, App
66	22	53.7	117	4	US-09-667-857-359	Sequence 359, App
67	22	53.7	232	4	US-09-702-705-993	Sequence 993, App
68	22	53.7	232	4	US-09-736-457-993	Sequence 993, App
69	22	53.7	232	4	US-09-614-124B-993	Sequence 993, App
70	22	53.7	232	4	US-09-678-824-993	Sequence 993, App
71	22	53.7	1529	3	US-09-189-760-5	Sequence 5, Appli
72	22	53.7	1529	3	US-09-188-811-5	Sequence 5, Appli
73	22	53.7	1529	3	US-09-514-422-5	Sequence 5, Appli
74	22	53.7	2199	4	US-09-708-725A-3	Sequence 3, Appli
75	22	53.7	2199	4	US-09-189-760-1	Sequence 1, Appli
76	22	53.7	2494	3	US-09-514-422-1	Sequence 1, Appli
77	22	53.7	2494	3	US-08-735-609-9	Sequence 9, Appli
78	22	53.7	3364	2	US-08-735-609-9	Sequence 9, Appli
79	22	53.7	3364	2	US-09-315-372-9	Sequence 9, Appli
80	22	53.7	3364	3	US-09-244-752-9	Sequence 9, Appli
81	22	53.7	3364	3	US-09-244-752-9	Sequence 9, Appli
82	22	53.7	3364	3	US-09-562-919-9	Sequence 9, Appli
83	22	53.7	3364	4	US-09-100-703A-55	Sequence 25, Appli
84	22	53.7	5230	4	US-09-838-718A-5	Sequence 26, Appli
85	22	53.7	5230	4	US-09-100-703A-5	Sequence 5, Appli
86	22	53.7	5231	4	US-09-100-703A-7	Sequence 27, Appli
87	22	53.7	5231	4	US-09-838-718A-7	Sequence 7, Appli
88	22	53.7	5270	4	US-09-838-718A-8	Sequence 8, Appli
89	22	53.7	5506	4	US-09-838-718A-6	Sequence 6, Appli
90	22	53.7	152331	3	US-09-128-155-17	Sequence 17, Appli
91	22	53.7	152331	3	US-09-128-155-17	Sequence 17, Appli
92	22	53.7	152331	3	US-09-751-389-3	Sequence 3, Appli
93	22	53.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli
94	22	53.2	228	4	US-09-621-976-8312	Sequence 8312, A
95	21.8	53.2	282	4	US-09-621-976-11262	Sequence 11262, A
96	21.8	53.2	284	4	US-09-621-976-11565	Sequence 1765, A
97	21.8	53.2	366	4	US-09-248-796A-1728	Sequence 1728, Ap
98	21.8	53.2	1281	4	US-09-134-000C-1175	Sequence 3175, Ap
99	21.8	53.2	1281	4	US-09-134-000C-1175	Sequence 3175, Ap
100	21.8	53.2	1281	4	US-09-134-000C-3273	Sequence 3273, Ap

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 Seconds
(without alignments)
1214.152 Million cell updates/sec

Title: US-10-035-833A-7073
Perfect score: 1 tcagcaagaagaaaaaa.....gccagccaagcttaatta 41
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 segs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: Genesegq_23Sep04:*
2: Genesegq1980s:*
3: Genesegq2000s:*
4: Genesegq2001as:*
5: Genesegq2001bs:*
6: Genesegq2002as:*
7: Genesegq2002bs:*
8: Genesegq2003as:*
9: Genesegq2003bs:*
10: Genesegq2003cs:*
11: Genesegq2003ds:*
12: Genesegq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	6	AB250291 Human cyt
2	41	100.0	5102	6	ABO75929 Human cyt
3	41	100.0	5102	6	ABK35488 Human end
4	41	100.0	5102	6	ABK62883 Breast ca
5	41	100.0	5102	6	ABK64720 Human ben
6	41	100.0	5102	6	ABK39861 Human all
7	41	100.0	5102	10	ADDD14611 Human src
8	41	100.0	5102	10	ACD46768 Human COP
9	41	100.0	5102	11	AD1332100 Human CNV
10	41	100.0	5128	6	ABV78036 Hypoxia-r
11	41	100.0	5128	6	ABV77942 Hypoxia-1
12	41	100.0	5128	8	ACF34492 Gene enco
13	41	100.0	5128	8	ACCS0124 Breast ca
14	41	100.0	5128	12	ADN03862 Antipsori
15	41	100.0	5134	6	ABK88882 Human CYP
16	41	100.0	5329	6	ABK94902 Human DNA
17	41	100.0	10254	6	ABN81206 Human CYP
18	40.6	99.0	3785	3	AAFL18025 Lung can
19	36.2	88.3	362	9	ACH31049 Human bon
20	27.8	67.8	11130	5	ABA16386 Human ner
21	27.6	67.3	23415	9	ADA02543 Mouse Pim

22	27.6	67.3	23415	10	ADB72281	ADB72281 Mouse Pim
23	27.6	67.3	23415	10	ADB59791	ADB59791 Mouse Pim
24	27	65.9	83450	10	AAD58977	AAD58977 Human pho
25	27	65.9	83450	10	ADG68582	ADG68582 Human pho
26	26.8	65.4	378	5	AAF66163	AAF66163 Novel hum
27	26.6	64.9	15832	6	ABK45396	ABK45396 Chemically
28	26.6	64.9	15832	6	ABL33342	ABL33342 Human imm
29	26.6	64.9	15832	6	ABK28243	ABK28243 DNA trans
30	26.4	64.4	765	4	ABL19958	ABL19958 Human bre
31	26	63.4	9261	9	ADA02544	ADA02544 Mouse Pim
32	26	63.4	9261	10	ADB72282	ADB72282 Mouse Pim
33	26	63.4	9261	10	ADB59792	ADB59792 Mouse DNA
34	25.6	62.4	110000	6	ABK55320.2	ABK55320.2 of
35	25.6	62.4	18399	6	ABP92831	ABP92831 Human ABC
36	25.6	62.4	18399	6	ABK55200	ABK55200 Genomic D
37	25.4	62.0	34151	6	ACH25351	ACH25351 Human adu
38	25.4	62.0	413	9	AAH35461	AAH35461 Arabidops
39	25.4	62.0	670	3	AAH35461	AAH35461 Arabidops
40	25.4	62.0	177851	8	AAH57272	AAH57272 bA438B23-
41	25.2	61.5	457	4	AAK71707	AAK71707 Human imm
42	25.2	61.5	633	10	ABK237826	ABK237826 N. gonorr
43	25.2	61.5	633	12	ADP83382	ADP83382 Breast sp
44	25.2	61.5	5263	12	ADP83382	ADP83382 Breast sp
45	25.2	61.5	42488	4	AAK66772	AAK66772 Human imm
46	25.2	61.0	2518	4	ADD48365	ADD48365 Human gen
47	25	61.0	27780	6	ABK12674	ABK12674 Selectin
48	25	61.0	40954	10	ADC85349	ADC85349 Mouse Sel
49	25	61.0	40955	9	ADA02870	ADA02870 Human SEL
50	25	61.0	40955	10	ADB72608	ADB72608 Human SEL
51	25	61.0	40955	12	ADW74465	ADW74465 Human car
52	25	61.0	9686	12	AD180019	AD180019 Human tra
53	25	61.0	13816	3	AAA34791	AAA34791 Human ade
54	25	61.0	141586	11	ABD20695	ABD20695 Human pul
55	25	61.0	141589	3	AAA35005	AAA35005 Human ade
56	25	61.0	141589	3	AAA35030	AAA35030 Human ade
57	25	61.0	141589	3	AAK21152	AAK21152 Human low
58	25	61.0	141589	3	AAK20913	AAK20913 Human ELA
59	25	61.0	141589	3	AAK21127	AAK21127 Human low
60	25	61.0	141589	10	ABZ96821	ABZ96821 Human nuc
61	25	61.0	141589	10	ABZ96607	ABZ96607 Human ELA
62	25	61.0	141589	10	ABZ96846	ABZ96846 Human nuc
63	25	61.0	141589	11	ABD20670	ABD20670 Human pul
64	25	61.0	141589	11	ABD19162	ABD19162 Human ELA
65	25	61.0	146982	11	ABD297136	ABD297136 Human ELA
66	25	61.0	146982	11	ABD19160	ABD19160 Human ELA
67	25	61.0	146982	11	AAK21437	AAK21437 Human fac
68	25	61.0	209273	10	ABZ97131	ABZ97131 Human enz
69	25	61.0	209274	11	ABD17970	ABD17970 Human fac
70	24.8	60.5	427	6	ABN78177	ABN78177 Human ORF
71	24.8	60.5	497	9	ACH28647	ACH28647 Human adu
72	24.8	60.5	11209	6	ABN80137	ABN80137 Human che
73	24.6	60.0	392	8	ABK54355	ABK54355 Bovine ES
74	24.6	60.0	2869	4	ABL18644	ABL18644 Human gen
75	24.6	60.0	3254	4	ABL18628	ABL18628 Drosophill
76	24.6	60.0	4592	10	ADDE62122	ADDE62122 Human gen
77	24.6	60.0	4592	10	ADDE61186	ADDE61186 Human gen
78	24.6	60.0	4592	10	ADDE62114	ADDE62114 Human gen
79	24.6	60.0	4592	10	ADDE62118	ADDE62118 Human gen
80	24.6	60.0	4592	10	ADDE61413	ADDE61413 Human gen
81	24.6	60.0	4592	10	ADDE61130	ADDE61130 Human gen
82	24.6	60.0	5081	8	ABT17798	ABT17798 Aspergill
83	24.6	60.0	5311	8	ABT19612	ABT19612 Aspergill
84	24.6	60.0	14487	4	ABL20344	ABL20344 Drosophill
85	24.6	60.0	14768	4	ABL10258	ABL10258 Drosophill
86	24.6	60.0	16838	6	AAH16687	AAH16687 DNA encod
87	24.6	60.0	16838	6	ACH74711	ACH74711 Human gen
88	24.4	59.5	500	12	AAH94030	AAH94030 Human neu
89	24.4	59.5	829	8	AAH94030	AAH94030 Human neu
90	24.4	59.5	1119	8	AAH94030	AAH94030 Human neu
91	24.4	59.5	3587	4	AAK93480	AAK93480 Human ful
92	24.4	59.5	3587	12	ADL31899	ADL31899 Full leng
93	24.4	59.5	4207	8	ACC46611	ACC46611 Human dit
94	24.4	59.5	6849	4	AAK72645	AAK72645 Human imm

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 720.113 seconds
(without alignments)
2692.464 Million cell updates/sec

Title: US-10-035-833a-7073
Perfect score: 41
Sequence: 1 tcagcaagaataaaaaaa.....gccagccagcttaatta 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: gb_da:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	41	100.0	2181	6 AX666080 Sequence
2	41	100.0	2721	6 AX666082 Sequence
3	41	100.0	3118	6 AX666089 Sequence
4	41	100.0	5102	6 BD176699 Sequence
5	41	100.0	5102	6 AR380881 Sequence
6	41	100.0	5102	6 AX330711 Sequence
7	41	100.0	5102	6 AX663644 Sequence
8	41	100.0	5102	6 BD168988 Sequence
9	41	100.0	5102	6 HSU03688 Sequence
10	41	100.0	5104	6 CO714214 Sequence
11	41	100.0	5134	6 AX666071 Sequence
12	41	100.0	5329	6 AX281748 Sequence
13	41	100.0	12124	9 AY393998 Homo sapi
14	41	100.0	12177	9 HSU56438 Homo sapi
15	41	100.0	79303	2 AC011074 Homo sapi
16	41	100.0	209156	9 AC009229 Homo sapi
17	41	100.0	211222	2 AC020097 Homo sapi
18	40	97.6	41	6 AX520875 Sequence
19	30.4	74.1	139130	9 AC091504 Pan trogl

20	29.6	72.2	245182	2 AC145940 Pan trogl
21	29.2	71.2	135119	2 AC011578 Homo sapi
22	29.2	71.2	158817	2 AC015398 Homo sapi
23	29	70.7	3124	11 G06772 Human SIS W
24	29	70.7	5234	11 BV177879 Bv177879 sqm97309
25	28.6	69.8	219335	9 AC005015 Homo sapi
26	28.6	69.8	219335	9 AC005015 Homo sapi
27	28.4	69.8	174480	9 AC083903 Homo sapi
28	28.2	68.8	139267	8 AC144592 Homo sapi
29	28.2	68.8	183104	9 AL355601 Homo sapi
30	28.2	68.8	208026	9 AP006292 Homo sapi
31	28.2	68.8	219555	2 AC133729 Rattus no
32	28.2	68.8	225612	2 AC117641 Mus muscu
33	28.2	68.8	310091	2 AC116258 Rattus no
34	27.8	67.8	133336	2 AF215842 Homo sapi
35	27.8	67.8	135572	9 AL133384 Homo sapi
36	27.8	67.8	170241	9 AC083967 Homo sapi
37	27.6	67.3	23415	6 AX695434 Homo sapi
38	27.4	66.8	87943	9 AC095064 Homo sapi
39	27.4	66.8	154002	10 AL662902 Mouse DNA
40	27.4	66.8	178495	2 BX510329 Danio rer
41	27.2	66.3	115911	9 AC093019 Homo sapi
42	27.2	66.3	120477	2 AL355995 Homo sapi
43	27.2	66.3	134764	2 AF003305 Homo sapi
44	27.2	66.3	155752	2 AC027557 Homo sapi
45	27.2	66.3	162731	2 BX323452 Danio rer
46	27.2	66.3	187728	2 AC062011 Homo sapi
47	27.2	66.3	190441	2 AC129960 Bos tauru
48	27.2	66.3	192001	2 AC019139 Homo sapi
49	27	65.9	41617	9 AL603841 Homo sapi
50	27	65.9	66928	2 AC125473 Homo sapi
51	27	65.9	83450	6 AR307588 Sequence
52	27	65.9	83450	6 AR475456 Sequence
53	27	65.9	102926	9 AC090829 Homo sapi
54	27	65.9	110000	2 BX324168 -1
55	27	65.9	123029	9 AF212832 Homo sapi
56	27	65.9	179400	9 AC087481 Homo sapi
57	27	65.9	181558	2 AC068301 Homo sapi
58	27	65.9	187647	2 AC073220 Homo sapi
59	27	65.9	189207	9 AC103706 Homo sapi
60	27	65.9	196179	2 AC150717 Callithri
61	27	65.9	250519	2 AC094894 Rattus no
62	27	65.9	257860	2 AC127719 Rattus no
63	27	65.9	328117	2 AC017097 Homo sapi
64	26.8	65.4	378	6 AX071447 Sequence
65	26.8	65.4	60310	9 AL391647 Human DNA
66	26.8	65.4	66224	9 AC073884 Homo sapi
67	26.8	65.4	112602	2 AC136797 Rattus no
68	26.8	65.4	136949	10 AL845271 Mouse DNA
69	26.8	65.4	152974	9 AL591073 Human DNA
70	26.8	65.4	174496	2 AC073070 Homo sapi
71	26.8	65.4	195443	2 AC134594 Mus muscu
72	26.8	65.4	209785	2 AC109497 Mus muscu
73	26.8	65.4	234724	10 AL683854 Mouse DNA
74	26.6	64.9	15832	6 AX277942 Sequence
75	26.6	64.9	15832	6 AX323629 Sequence
76	26.6	64.9	15832	6 AX346244 Sequence
77	26.6	64.9	43147	6 AP002955 Homo sapi
78	26.6	64.9	83922	8 T9A4 AR096773 Arabidops
79	26.6	64.9	99856	8 AF724G24 Arabidops
80	26.6	64.9	142948	9 AC147025 Arabidops
81	26.6	64.9	199236	2 AC109237 Pan trogl
82	26.6	64.9	199861	8 ATCHRI29 Mus muscu
83	26.6	64.9	207890	2 AC102551 Arabidops
84	26.6	64.9	221879	2 AC096704 Mus muscu
85	26.6	64.9	225757	2 AC094658 Rattus no
86	26.6	64.9	252737	2 AC095976 Rattus no
87	26.6	64.4	272137	6 AC027391 Rattus no
88	26.4	64.4	4081	9 HSU806464 Homo sapi
89	26.4	64.4	14771	10 AL929432 Mouse DNA
90	26.4	64.4	27543	9 AB126081 Homo sapi
91	26.4	64.4	82059	9 AC130896 Homo sapi
92	26.4	64.4	123520	9 HSU447821 Human DNA

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1417.45 Seconds
(without alignments)
1028.317 Million cell updates/sec

Title: US-10-035-833A-7071

Perfect score: 40
Sequence: 1 agctctggagagatcttttgtagtcaagacttaagggc 40

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hnc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	40	100.0	717	5	EM997179	EM997179 UI-H-ED0-
2	39	97.5	630	5	EM995447	EM995447 UI-H-ED0-
3	35.4	88.5	627	6	CB851415	CB851415 UI-CF-DU1
4	34	85.0	958	5	BO723128	BO723128 ACENCOURT
5	29	72.5	403	6	CA123715	CA123715 K-EST0172
6	29	72.5	579	6	CB160042	CB160042 K-EST0219
7	29	72.5	592	1	AV717361	AV717361 AV717361
8	29	72.5	595	1	EM713769	EM713769 UI-E-ED0-
9	29	72.5	721	4	EM676467	EM676467 UI-E-ED0-
10	29	72.5	934	4	BG115583	BG115583 602284061
11	28	70.0	707	5	BO020105	BO020105 UI-H-ED0-
12	27.8	69.5	465	5	BO689794	BO689794 UI-CF-FNO
13	25.8	64.5	1270	8	BZ555833	BZ555833 Pacc1-60-
14	25.2	63.0	391	1	AI974443	AI974443 T110391e-
15	24.8	62.0	793	4	BG78374	BG78374 60266527
16	24.2	60.5	953	9	CNS03X9A	CNS03X9A Tetraodon
17	23.8	59.5	458	3	CB653825	CB653825 Tetraodon
18	23.8	59.5	796	8	BZ450004	BZ450004 BONEV88TR
19	23.8	59.5	1056	3	CB634022	CB634022 Tetraodon
20	23.8	59.5	1091	3	CB649663	CB649663 Tetraodon
21	23.8	59.5	1117	3	CB634278	CB634278 Tetraodon
22	23.8	59.5	1125	3	CB637710	CB637710 Tetraodon
23	23.8	59.5	1167	3	CB655543	CB655543 Tetraodon
24	23.8	59.5	1170	3	CB649639	CB649639 Tetraodon

25	23.8	59.5	1171	3	CB635466	CB635466 Tetraodon
26	23.8	59.5	1174	3	CB641445	CB641445 Tetraodon
27	23.8	59.5	1200	3	CB640695	CB640695 Tetraodon
28	23.8	59.5	1202	3	CB645853	CB645853 Tetraodon
29	23.8	59.5	1219	3	CB644557	CB644557 Tetraodon
30	23.6	59.0	464	6	CA557970	CA557970 K0235H03-
31	23.6	59.0	591	7	CN701987	CN701987 E0456G01-
32	23.6	59.0	595	7	CN530307	CN530307 UI-M-H00-
33	23.6	59.0	635	7	CN698454	CN698454 E0408A10-
34	23.6	59.0	635	7	CN530701	CN530701 UI-M-H00-
35	23.6	59.0	681	7	CF735941	CF735941 UI-M-H00-
36	23.6	59.0	705	7	BI250633	BI250633 603312046
37	23.6	59.0	802	4	BI250633	BI250633 602993702
38	23.6	59.0	813	4	BZ208073	BZ208073 CH230-330
39	23.6	59.0	862	6	BZ208073	BZ208073 CH230-330
40	23.4	58.5	485	4	BI403019	BI403019 MT-P-CP1-
41	23.2	58.0	213	9	CE673711	CE673711 t1gr-gss-
42	23.2	58.0	282	9	AL765831	AL765831 At2idicps
43	23.2	58.0	622	8	BH732308	BH732308 BOMFB60TR
44	23.2	58.0	671	9	CR206141	CR206141 Reverse s
45	23.2	58.0	1436	9	CL647577	CL647577 CH213-142
46	23	57.5	701	8	CC073395	CC073395 CSU-K33F.
47	23	57.5	782	4	B6620617	B6620617 602619787
48	23	57.5	1029	2	B5885694	B5885694 601508903
49	22.8	57.0	300	8	AQ261554	AQ261554 C1TBI-E1-
50	22.8	57.0	517	8	AQ195502	AQ195502 RPT11-60
51	22.8	57.0	745	9	CL009111	CL009111 ZMMBBD054
52	22.8	57.0	800	8	BZ526318	BZ526318 OGAKC47C
53	22.8	57.0	852	8	BZ533595	BZ533595 OGAKB93TC
54	22.8	57.0	862	8	CC584881	CC584881 CH240-381
55	22.8	57.0	865	9	CC263798	CC263798 CH261-211
56	22.6	56.5	431	8	B58718	B58718 CTT-HSP-201
57	22.6	56.5	443	8	BZ265295	BZ265295 CH230-274
58	22.6	56.5	447	8	AZ268949	AZ268949 RPT1-23-1
59	22.6	56.5	456	8	AQ228961	AQ228961 HS_2013_B
60	22.6	56.5	483	8	B66674	B66674 CTT-HSP-201
61	22.6	56.5	513	8	AZ789872	AZ789872 2M0038012
62	22.6	56.5	560	1	A1897462	A1897462 EST766805
63	22.6	56.5	575	1	A1486819	A1486819 EST45141
64	22.6	56.5	578	9	CC956674	CC956674 BO1A15TF
65	22.6	56.5	591	5	BO551403	BO551403 H4009A11-
66	22.6	56.5	659	1	AL643034	AL643034 AL643034
67	22.6	56.5	658	8	BH511990	BH511990 B0HSM52TR
68	22.6	56.5	672	7	CF742552	CF742552 UI-M-HR0-
69	22.6	56.5	685	7	CN081464	CN081464 EC2BBA19C
70	22.6	56.5	695	8	AZ087760	AZ087760 RPT1-23-3
71	22.6	56.5	697	9	AG330950	AG330950 Mus muscu
72	22.6	56.5	714	1	AL650479	AL650479 AL650479
73	22.6	56.5	733	8	BH604717	BH604717 B0HTW47TF
74	22.6	56.5	740	8	AQ307280	AQ307280 HS_2013_A
75	22.6	56.5	771	9	CG030035	CG030035 PUTK098TD
76	22.6	56.5	832	5	B0839601	B0839601 AGENCOURT
77	22.6	56.5	862	8	BZ975451	BZ975451 PUGJA31TB
78	22.6	56.5	865	8	BZ975457	BZ975457 PUGJA31TB
79	22.6	56.5	877	5	B0899871	B0899871 AGENCOURT
80	22.6	56.5	893	5	CG444808	CG444808 OGSEEL17TV
81	22.6	56.5	910	8	CC387817	CC387817 PUMBJ13TD
82	22.6	56.5	914	9	CG230657	CG230657 OGWG083TH
83	22.6	56.5	915	9	CG770721	CG770721 TCBA3-2C
84	22.6	56.5	942	9	CG544472	CG544472 PUK161TD
85	22.6	56.5	985	4	BG504138	BG504138 602552663
86	22.6	56.5	1180	8	CC277420	CC277420 CH261-67N
87	22.6	56.5	1198	8	AG441632	AG441632 Mus muscu
88	22.4	56.0	315	8	AQ982177	AQ982177 RPT1-23-4
89	22.4	56.0	364	8	AZ051795	AZ051795 RPT1-23-1
90	22.4	56.0	384	8	AZ299952	AZ299952 RPT1-23-1
91	22.4	56.0	488	8	AZ554047	AZ554047 ZM0219L004
92	22.4	56.0	581	8	BZ095200	BZ095200 CH230-221
93	22.4	56.0	598	8	CE347992	CE347992 t1gr-gss-
94	22.4	56.0	627	8	AG974475	AG974475 RPT1-23-3
95	22.4	56.0	642	8	BH054555	BH054555 RPT1-24-2
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 ; Search time 154.902 Seconds
(without alignments)
1324.090 Million cell updates/sec

Title: US-10-035-833a-7071
Perfect score: 40
Sequence: 1 agctctggagatttttcagctcaagaactaaaggac 40

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 segs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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7	40	100.0	3785	9	US-09-925-302-44
8	40	100.0	5102	9	US-09-919-497-8
9	40	100.0	5102	9	US-09-954-531-153
10	40	100.0	5102	10	US-09-960-706-938
11	40	100.0	5102	10	US-09-873-319-615
12	40	100.0	5102	15	US-10-204-752-36

13	40	100.0	5102	16	US-10-641-643-1426
14	40	100.0	5102	17	US-10-775-169-230
15	40	100.0	5128	15	US-10-177-229-96
16	40	100.0	5128	15	US-10-170-385-138
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18	40	100.0	5128	15	US-10-170-385-138
19	40	100.0	5128	15	US-10-172-118-433
20	40	100.0	5134	10	US-10-342-887-433
21	40	100.0	5134	10	US-09-999-686-11
22	37	92.5	307	16	US-10-242-538A-53750
23	37	92.5	307	16	US-10-083-789A-53750
24	29	72.5	41	16	US-10-035-833a-1245
25	29	72.5	41	16	US-10-035-833a-7070
26	28.8	72.0	174	9	US-10-240-965-157
27	28.8	72.0	192	9	US-09-783-590-8496
28	24.4	61.0	2129	9	US-09-822-830A-443
29	24	60.0	8349	15	US-10-311-455-1761
30	23.6	59.0	9464	9	US-09-738-847-1
31	23.6	59.0	9464	16	US-10-672-489-1
32	23.6	59.0	9464	16	US-10-673-023-1
33	23.6	59.0	9464	16	US-10-702-755-1
34	23.6	59.0	9464	17	US-10-673-008-1
35	23.2	58.0	507	16	US-10-424-599-126191
36	23	57.5	6191	15	US-10-311-455-1343
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38	22.4	56.0	2001	13	US-10-027-632-100363
39	22.4	56.0	2008	13	US-10-027-632-97455
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41	22.4	56.0	17703	16	US-10-257-166-34
42	22	55.0	550	16	US-10-621-901-2167
43	22	55.0	736	16	US-10-424-599-38471
44	22	55.0	4831	15	US-10-172-118-1509
45	22	55.0	4831	16	US-10-342-887-1509
46	21.8	54.5	679	13	US-10-027-632-302658
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69	21.4	53.5	367378	15	US-10-312-841-1
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 ; Search time 36.2745 Seconds.
(without alignments)
783.789 Million cell updates/sec

Title: US-10-035-833a-7071
Perfect score: 40
Sequence: 1 agctctgggagattttttgagtcgaagactaaaggac 40

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

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4	23.6	59.0	9464	US-09-738-847-1	Sequence 1, Appl
5	23.6	59.0	9464	US-09-378-810-1	Sequence 679, App
6	21	52.5	1083	US-09-543-681A-679	Sequence 1, Appl
7	21	52.5	1083	US-09-047-026A-1	Sequence 3, Appl
8	20.8	52.0	5992	US-08-475-891A-3	Sequence 31526, A
9	20.6	51.5	267	US-09-270-767-31526	Sequence 15186, A
10	20.6	51.5	417	US-09-270-767-31526	Sequence 2269, Ap
11	20.6	51.5	3534	US-09-134-001C-2269	Sequence 175, App
12	20.6	51.5	8339	US-08-956-171E-175	Sequence 175, App
13	20.6	51.5	8339	US-08-781-986A-175	Sequence 2813, Ap
14	20.4	51.0	832	US-09-621-976-2813	Sequence 1, Appl
15	20.4	51.0	1230025	US-09-198-452A-1	Sequence 1, Appl
16	20.2	50.5	406	US-09-621-976-13437	Sequence 10381, A
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18	20.2	50.5	1539	US-09-107-532A-2905	Sequence 32, Appl
19	20	50.0	576	US-09-288-143-32	Sequence 12442, A
20	20	50.0	1430	US-09-270-767-12442	Sequence 1, Appl
21	20	50.0	173	US-09-171-482-1	Sequence 11078, A
22	19.8	49.5	273	US-09-621-976-11078	Sequence 14296, A
23	19.8	49.5	356	US-09-621-976-14296	Sequence 12146, A
24	19.8	49.5	441	US-09-513-999C-12146	Sequence 2494, Ap
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26	19.8	49.5	2133	US-10-118-328-1	Sequence 17, Appl
27	19.8	49.5	2451	US-09-808-701A-17	Sequence 16, Appl
28	19.8	49.5	2499	US-09-808-701A-16	Sequence 3, Appl
29	19.8	49.5	30350	US-10-118-328-3	Sequence 23, Appl
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32	19.6	49.0	1001	US-08-641-638-455	Sequence 455, App
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34	19.6	49.0	1955	US-08-956-171E-598	Sequence 69, Appl
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80	19.2	47.5	955	US-08-016-434-76	Sequence 2617, Ap
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97	18.8	47.0	576	US-09-270-767-55247	Sequence 21718, A
98	18.8	47.0	642	US-09-270-767-11718	Sequence 1514, Ap
99	18.8	47.0	722	US-09-547-681A-1514	Sequence 9942, Ap
100	18.8	47.0	722	US-09-270-767-9942	Sequence 9942, Ap

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OM nucleic - nucleic search, using sw model

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1214.152 Million cell updates/sec

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9: Geneseg_20Oct04:*
10: Geneseg_20Oct04:*
11: Geneseg_20Oct04:*
12: Geneseg_20Oct04:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	100.0	40	6	ABZ44462 Human cyt
2	40	100.0	40	6	ABZ50289 Human cyt
3	40	100.0	3785	3	AA18025 Lung can
4	40	100.0	5102	6	ABO79929 Human cyt
5	40	100.0	5102	6	ABK35488 Human end
6	40	100.0	5102	6	ABK62883 Breast ca
7	40	100.0	5102	6	ABK64720 Human ben
8	40	100.0	5102	6	ABK64720 Human all
9	40	100.0	5102	10	AD14611 Human src
10	40	100.0	5102	10	AD14611 Human src
11	40	100.0	5102	11	AD14611 Human src
12	40	100.0	5102	11	AD14611 Human src
13	40	100.0	5102	6	ABV78036 Hypoxia-r
14	40	100.0	5102	6	ABV77942 Hypoxia-r
15	40	100.0	5102	8	ACF34492 Gene enco
16	40	100.0	5102	8	ACF34492 Breast ca
17	40	100.0	5102	12	ADN03862 Antipsof
18	40	100.0	5102	6	ABK88882 Human cyt
19	40	100.0	5102	6	ABN81206 Human cyt
20	40	100.0	5102	6	ABZ44461 Human cyt
21	40	100.0	5102	6	ABZ50288 Human cyt
22	40	100.0	5102	6	ABZ50288 Human cyt
23	40	100.0	5102	6	ABZ50288 Human cyt
24	40	100.0	5102	6	ABZ50288 Human cyt
25	40	100.0	5102	6	ABZ50288 Human cyt
26	40	100.0	5102	6	ABZ50288 Human cyt
27	40	100.0	5102	6	ABZ50288 Human cyt
28	40	100.0	5102	6	ABZ50288 Human cyt
29	40	100.0	5102	6	ABZ50288 Human cyt
30	40	100.0	5102	6	ABZ50288 Human cyt
31	40	100.0	5102	6	ABZ50288 Human cyt
32	40	100.0	5102	6	ABZ50288 Human cyt
33	40	100.0	5102	6	ABZ50288 Human cyt
34	40	100.0	5102	6	ABZ50288 Human cyt
35	40	100.0	5102	6	ABZ50288 Human cyt
36	40	100.0	5102	6	ABZ50288 Human cyt
37	40	100.0	5102	6	ABZ50288 Human cyt
38	40	100.0	5102	6	ABZ50288 Human cyt
39	40	100.0	5102	6	ABZ50288 Human cyt
40	40	100.0	5102	6	ABZ50288 Human cyt
41	40	100.0	5102	6	ABZ50288 Human cyt
42	40	100.0	5102	6	ABZ50288 Human cyt
43	40	100.0	5102	6	ABZ50288 Human cyt
44	40	100.0	5102	6	ABZ50288 Human cyt
45	40	100.0	5102	6	ABZ50288 Human cyt
46	40	100.0	5102	6	ABZ50288 Human cyt
47	40	100.0	5102	6	ABZ50288 Human cyt
48	40	100.0	5102	6	ABZ50288 Human cyt
49	40	100.0	5102	6	ABZ50288 Human cyt
50	40	100.0	5102	6	ABZ50288 Human cyt
51	40	100.0	5102	6	ABZ50288 Human cyt
52	40	100.0	5102	6	ABZ50288 Human cyt
53	40	100.0	5102	6	ABZ50288 Human cyt
54	40	100.0	5102	6	ABZ50288 Human cyt
55	40	100.0	5102	6	ABZ50288 Human cyt
56	40	100.0	5102	6	ABZ50288 Human cyt
57	40	100.0	5102	6	ABZ50288 Human cyt
58	40	100.0	5102	6	ABZ50288 Human cyt
59	40	100.0	5102	6	ABZ50288 Human cyt
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61	40	100.0	5102	6	ABZ50288 Human cyt
62	40	100.0	5102	6	ABZ50288 Human cyt
63	40	100.0	5102	6	ABZ50288 Human cyt
64	40	100.0	5102	6	ABZ50288 Human cyt
65	40	100.0	5102	6	ABZ50288 Human cyt
66	40	100.0	5102	6	ABZ50288 Human cyt
67	40	100.0	5102	6	ABZ50288 Human cyt
68	40	100.0	5102	6	ABZ50288 Human cyt
69	40	100.0	5102	6	ABZ50288 Human cyt
70	40	100.0	5102	6	ABZ50288 Human cyt
71	40	100.0	5102	6	ABZ50288 Human cyt
72	40	100.0	5102	6	ABZ50288 Human cyt
73	40	100.0	5102	6	ABZ50288 Human cyt
74	40	100.0	5102	6	ABZ50288 Human cyt
75	40	100.0	5102	6	ABZ50288 Human cyt
76	40	100.0	5102	6	ABZ50288 Human cyt
77	40	100.0	5102	6	ABZ50288 Human cyt
78	40	100.0	5102	6	ABZ50288 Human cyt
79	40	100.0	5102	6	ABZ50288 Human cyt
80	40	100.0	5102	6	ABZ50288 Human cyt
81	40	100.0	5102	6	ABZ50288 Human cyt
82	40	100.0	5102	6	ABZ50288 Human cyt
83	40	100.0	5102	6	ABZ50288 Human cyt
84	40	100.0	5102	6	ABZ50288 Human cyt
85	40	100.0	5102	6	ABZ50288 Human cyt
86	40	100.0	5102	6	ABZ50288 Human cyt
87	40	100.0	5102	6	ABZ50288 Human cyt
88	40	100.0	5102	6	ABZ50288 Human cyt
89	40	100.0	5102	6	ABZ50288 Human cyt
90	40	100.0	5102	6	ABZ50288 Human cyt
91	40	100.0	5102	6	ABZ50288 Human cyt
92	40	100.0	5102	6	ABZ50288 Human cyt
93	40	100.0	5102	6	ABZ50288 Human cyt
94	40	100.0	5102	6	ABZ50288 Human cyt

22	24.4	61.0	2169	6	AA62656	AA62656 CDNA sequ
23	24	60.0	251	2	AA11003	AA11003 Human bla
24	24	60.0	350	2	AA67238	AA67238 Human sin
25	24	60.0	8349	6	AB133788	AB133788 Human imm
26	23.8	59.5	11000	2	AA201425_07	Continuation (8 of
27	23.6	59.0	9464	4	AA65694	AA65694 Nucleotid
28	23.6	59.0	9467	4	AA299678	AA299678 DNA sequ
29	23	57.5	6191	6	AB133370	AB133370 Human imm
30	22.6	56.5	101	10	AD675927	AD675927 Tomato p1
31	22.6	56.5	2263	4	AB104390	AB104390 Drosophi
32	22.4	56.0	17703	6	ABK39953	ABK39953 Human che
33	22	55.0	350	12	AD111725	AD111725 Cat filea
34	22	55.0	744	10	ACF68467	ACF68467 Phototrab
35	22	55.0	4129	12	ADU72016	ADU72016 Human PMW
36	22	55.0	10264	10	ACF65378	ACF65378 Phototrab
37	22	55.0	110000	10	ACF67367_11	Continuation (12 o
38	22	55.0	110000	10	ACF67367_12	Continuation (13 o
39	21.8	54.5	597	5	ABV55315	ABV55315 Human pro
40	21.8	54.5	2000	8	ADA72396	ADA72396 Rice gene
41	21.8	54.5	6151	6	AB133610	AB133610 Human imm
42	21.8	54.5	6151	6	ABK28275	ABK28275 DNA trans
43	21.6	54.0	569	4	AAH10768	AAH10768 Human CDN
44	21.6	54.0	1833	4	AAH15049	AAH15049 Human CDN
45	21.6	54.0	3752	6	ABK13001	ABK13001 DNA encod
46	21.6	54.0	12301	5	AAK34544	AAK34544 Human DNA
47	21.6	54.0	96599	10	ADC85298	ADC85298 Human Bgr
48	21.6	54.0	96600	9	ADA02819	ADA02819 Mouse Sbs
49	21.6	54.0	96600	10	ADA02819	ADA02819 Mouse Sbs
50	21.6	54.0	96600	12	ADM74414	ADM74414 Murine ca
51	21.4	53.5	6215	2	AAO59549	AAO59549 Human bra
52	21.4	53.5	6215	6	AB132126	AB132126 Human imm
53	21.4	53.5	6215	6	ABN79998	ABN79998 Human che
54	21.4	53.5	6282	4	AAK45421	AAK45421 Chemi
55	21.4	53.5	7537	4	ABL09602	ABL09602 Drosophi
56	21.4	53.5	8440	6	ABK28346	ABK28346 DNA trans
57	21.4	53.5	15430	4	AAK70953	AAK70953 Human imm
58	21.4	53.5	110000	10	ADH10017_1	Continuation (2 of
59	21.2	53.0	363	2	AA226219	AA226219 Human gen
60	21.2	53.0	373	4	AA166690	AA166690 Human pol
61	21.2	53.0	373	4	ADL36869	ADL36869 Human ova
62	21.2	53.0	573	5	AD171714	AD171714 Human ova
63	21.2	53.0	573	5	AD143253	AD143253 Human ova
64	21.2	53.0	1547	5	ADL45316	ADL45316 Human ova
65	21.2	53.0	5722	6	ABK31441	ABK31441 Signal tr
66	21.2	53.0	5722	6	AB170416	AB170416 Chemi
67	21.2	53.0	5722	6	AA661359	AA661359 Human gen
68	21.2	53.0	100267	6	AB111032	AB111032 Human bre
69	21.2	52.5	427	8	ABX43206	ABX43206 Bovine ES
70	21	52.5	480	3	AAK53860	AAK53860 Arabidops
71	21	52.5	589	3	AAK53462	AAK53462 Arabidops
72	21	52.5	1040	6	AB076438	AB076438 S. cerevi
73	21	52.5	1083	10	ADP00394	ADP00394 Bacteri
74	21	52.5	1565	3	AAK37656	AAK37656 Arabidops
75	21	52.5	2154	12	ADK67445	ADK67445 Baker's y
76	21	52.5	4125	3	AAK50716	AAK50716 Arabidops
77	21	52.5	4906	3	AAZ45133	AAZ45133 Saccharom
78	21	52.5	28564	10	ADD48770	ADD48770 Human gen
79	21	52.5	53585	2	AAK20251	AAK20251 Borrelia
80	21	52.5	93000	12	AD079405	AD079405 CENP
81	21	52.5	110000	2	AAK20248_04	Continuation (5 of
82	21	52.5	116277	2	AAK20248	AAK20248 Borrelia
83	21	52.5	190000	10	ADL13752	ADL13752 Osteoarth
84	21	52.5	210204	12	ADQ18927	ADQ18927 Human sof
85	20.8	52.0	366	4	AAI91908	AAI91908 Human pol
86	20.8	52.0	431	10	ADP80704	ADP80704 Leukaemia
87	20.8	52.0	439	5	ABV52027	ABV52027 Human pro
88	20.8	52.0	679	3	AAK44003	AAK44003 Arabidops
89	20.8	52.0	829	3	AAK02702	AAK02702 Human col
90	20.8	52.0	2183	4	AAK51899	AAK51899 Human pol
91	20.8	52.0	4897	12	ADJ12544	ADJ12544 DNA fragm
92	20.8	52.0	4908	10	ADP82102	ADP82102 Leukaemia
93	20.8	52.0	4908	10	ADP82101	ADP82101 Leukaemia
94	20.8	52.0	4908	10	ADP82100	ADP82100 Leukaemia

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CM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 702.549 Seconds
(without alignments)
2692.464 Million cell updates/sec

Title: US-10-035-833a-7071

Perfect score: 1 agctctcgagagatttttttgagtcagaagcttaagggc 40

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_ptg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_ptg: *
7: gb_ph: *
8: gb_pl: *
9: gb_dr: *
10: gb_ro: *
11: gb_ste: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	40	6	AX515048
2	40	100.0	40	6	AX515048 Sequence
3	40	100.0	2181	6	AX520873 Sequence
4	40	100.0	2799	6	AX666080 Sequence
5	40	100.0	3118	6	BC012049 Homo sapi
6	40	100.0	3124	11	G067722
7	40	100.0	5102	6	BD176699
8	40	100.0	5102	6	AR380881
9	40	100.0	5102	6	AX330711 Sequence
10	40	100.0	5102	6	AX663644 Sequence
11	40	100.0	5102	6	BD169898
12	40	100.0	5102	6	HSU03668
13	40	100.0	5104	6	CO714214
14	40	100.0	5134	6	AX666071
15	40	100.0	5234	11	BV177879
16	40	100.0	12177	9	HSU56438
17	40	100.0	79303	2	AC011074
18	40	100.0	209156	2	AC009229
19	40	100.0	211222	2	AC022097

20	37	92.5	307	6	CO708824	CO708824 Sequence
21	29	72.5	41	6	AX515047	AX515047 Sequence
22	29	72.5	41	6	AX520872	AX520872 Sequence
23	29	72.5	1596	6	AF450130S3	AF450130 Homo sapi
24	29	72.5	5329	6	AX281748	AX281748 Sequence
25	29	72.5	12124	9	AX393998	AX393998 Homo sapi
26	26	65.5	84742	2	AC099937	AC099937 Mus muscu
27	25	62.5	180835	2	BX957237	BX957237 Dario rer
28	24	60.5	165964	2	AC128313	AC128313 Homo sapi
29	24	60.5	195545	2	AC121701	AC121701 Rattus no
30	24	60.5	214363	2	AC109876	AC109876 Rattus no
31	24	60.5	234450	2	AC132162	AC132162 Rattus no
32	24	60.5	237462	2	AC097120	AC097120 Rattus no
33	24	60.0	8349	6	AX346690	AX346690 Sequence
34	24	60.0	163399	10	AL671920	AL671920 Mouse DNA
35	24	60.0	203953	10	AC087560	AC087560 Mus muscu
36	24	60.0	228059	2	AC109886	AC109886 Rattus no
37	24	60.0	275742	2	AC096514	AC096514 Rattus no
38	23	59.5	12088	1	AE001334	AE001334 Chlamydia
39	23	59.5	128965	9	AL357562	AL357562 Human DNA
40	23	59.5	146275	2	AC080119	AC080119 Homo sapi
41	23	59.5	150026	2	AL589868	AL589868 Homo sapi
42	23	59.5	199894	2	AC149799	AC149799 Aedes aeg
43	23	59.5	234795	2	AL391236	AL391236 Homo sapi
44	23	59.5	236203	2	AC096613	AC096613 Rattus no
45	23	59.5	335695	2	AC111623	AC111623 Rattus no
46	23	59.0	4373	10	BC076615	BC076615 Mus muscu
47	23	59.0	6345	10	D83033	D83033 Mouse mRNA
48	23	59.0	9464	6	E43300	E43300 Sequence
49	23	59.0	9464	6	AR441877	AR441877 Position
50	23	59.0	9464	6	AR490814	AR490814 Sequence
51	23	59.0	9464	6	AL133804	AL133804 Sequence
52	23	59.0	32679	3	CE120D3	CE120D3 Caenorhabdi
53	23	59.0	158861	10	AL845273	AL845273 Mouse DNA
54	23	59.0	163640	9	AC093328	AC093328 Homo sapi
55	23	59.0	167794	2	AF215844	AF215844 Homo sapi
56	23	59.0	167710	9	AL591463	AL591463 Human DNA
57	23	59.0	226460	10	AC098730	AC098730 Mus muscu
58	23	59.0	223041	2	AC113842	AC113842 Rattus no
59	23	59.0	257396	2	AC095924	AC095924 Rattus no
60	23	59.0	268912	2	AC094291	AC094291 Rattus no
61	23	58.0	826	8	AF124833	AF124833 Malus dom
62	23	58.0	87967	8	AC005223	AC005223 Arabidops
63	23	58.0	137749	2	AC109361	AC109361 Homo sapi
64	23	58.0	181401	2	AL954127	AL954127 Mus muscu
65	23	58.0	186547	10	AL772166	AL772166 Mouse DNA
66	23	58.0	189876	9	AL357892	AL357892 Human DNA
67	23	58.0	227477	2	AC097083	AC097083 Rattus no
68	23	58.0	248510	2	AC095814	AC095814 Rattus no
69	23	58.0	254381	2	AC128342	AC128342 Rattus no
70	23	58.0	285107	2	AC103104	AC103104 Rattus no
71	23	57.5	687	5	CR389425	CR389425 Gallus ga
72	23	57.5	6191	6	AX346272	AX346272 Sequence
73	23	57.5	25305	3	CE735C8	CE735C8 Caenorhabdi
74	23	57.5	79284	2	EX927314	EX927314 Dario rer
75	23	57.5	155255	9	AL103893	AL103893 Papio anu
76	23	57.5	166870	9	CNS05TEP	AL159228 Human chr
77	23	57.5	194433	9	HSBA425MS	AL109614 Human chr
78	23	57.5	299700	1	AP006571	AP006571 Gloeobact
79	23	57.0	517	11	G61210	G61210 SHGC-85518
80	23	57.0	70095	2	AC149156	AC149156 Xenopus t
81	23	57.0	73227	2	AC022587	AC022587 Homo sapi
82	23	57.0	106363	9	AL662788	AL662788 Human DNA
83	23	57.0	110000	10	AE014177_2	AE014177 Contiguation (3 of
84	23	57.0	111762	9	AC103851	AC103851 Homo sapi
85	23	57.0	118271	9	HSJ18113	AL096801 Human DNA
86	23	57.0	121094	10	AL928667	AL928667 Mouse DNA
87	23	57.0	125147	2	AC074081	AC074081 Homo sapi
88	23	57.0	143331	10	AC122058	AC122058 Mus muscu
89	23	57.0	149109	2	AC023181	AC023181 Homo sapi
90	23	57.0	149252	2	AC066580	AC066580 Homo sapi
91	23	57.0	150180	2	AL512350	AL512350 Homo sapi
92	23	57.0	165667	2	CR392342	CR392342 Dario rer

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:11:10 ; Search time 1452.89 Seconds
(without alignments)
1028.317 Million cell updates/sec

Title: US-10-035-833a-7064

Perfect score: 41
Sequence: 1 tgcagcagcacttaccaccta.....ttctctctgattttgagtca 41

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hrc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	99.0	775	8	AQ740902 HS.2274.A
2	25.8	62.9	832	2	BE967994 603287713
3	24.6	60.0	545	5	BM961466 c1A1K207
4	24.2	59.0	377	8	AZ046892 nbeD0088L
5	24.2	59.0	753	9	CL610449 OR_BBA000
6	23.6	58.5	758	2	CR239831 Reverse s
7	23.6	57.6	262	2	BB718435 BB718435
8	23.6	57.6	379	5	BQ703520 EST68.alm
9	23.6	57.6	560	2	AM642665 cm21c01.w
10	23.6	57.6	599	2	AM329910 TENU4717
11	23.6	57.6	638	9	AG017891 Homo sapi
12	23.6	57.6	645	9	AG017885 Homo sapi
13	23.6	57.6	742	5	BU219688 603750155
14	23.6	57.6	964	9	CNS035UP
15	23.4	57.1	430	8	AZ035357 RCT1-23-2
16	23.4	57.1	782	7	CK359869 AGENCOURT
17	23.4	56.6	215	6	CD946458 REX 95 Ge
18	23.4	56.1	409	2	BE607500
19	23.4	56.1	429	2	AM934665
20	23.4	56.1	502	4	BG551297 E8d35G04.
21	23.4	56.1	517	2	BE449596 EST356355
22	23.4	56.1	534	8	B2837488 CH240.248
23	23.4	56.1	569	5	B0094749 san51c01.
24	23.4	56.1	614	5	BU926165 sas87c06.

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 09:56:20 : Search time 158.775 Seconds
(without alignments)
1324.090 Million cell updates/sec

Title: US-10-035-833A-7064

Percent score: 41
Sequence: 1 tgcagcactaccaccta.....ttccctcgtatttgatca 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800528 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications_NA: *
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	99.0	41	US-10-035-833A-1239	Sequence 1239, App
2	40.6	99.0	41	US-10-035-833A-7064	Sequence 7064, App
3	31.4	76.6	5735	US-10-257-166-148	Sequence 148, App
4	24.2	50.0	2694	US-10-437-963-18752	Sequence 78752, A
5	23.4	57.1	759	US-10-027-632-173535	Sequence 173535,
6	23.4	57.1	759	US-10-027-632-173535	Sequence 173535,
7	23	56.1	5735	US-10-257-166-147	Sequence 147, App
8	22.8	55.6	133300	US-10-331-053-70	Sequence 70, App
9	22.8	55.6	169407	US-10-331-053-70	Sequence 305, App
10	22.2	54.1	392	US-10-424-599-48033	Sequence 48033, A
11	22.2	54.1	470	US-09-764-870-645	Sequence 645, App
12	22.2	54.1	470	US-10-125-540-645	Sequence 645, App

13	22	53.7	197526	US-10-322-281-498	Sequence 498, App
14	21.8	53.2	47322	US-10-322-281-507	Sequence 507, App
15	21.6	52.7	3863	US-10-172-118-79	Sequence 79, App
16	21.6	52.7	3863	US-10-342-887-79	Sequence 79, App
17	21.6	52.7	44763	US-10-741-601-5563	Sequence 553, App
18	21.2	51.7	80376	US-10-041-018-376	Sequence 376, App
19	21	51.2	554	US-10-027-632-290326	Sequence 290326,
20	21	51.2	554	US-10-027-632-290326	Sequence 290326,
21	21	51.2	1199	US-10-424-599-57900	Sequence 57900, A
22	21	51.2	32404	US-09-597-722-160	Sequence 160, App
23	20.8	50.7	775	US-10-424-599-24445	Sequence 24445, A
24	20.8	50.7	1731	US-09-861-132-485	Sequence 485, App
25	20.8	50.7	1731	US-09-861-132-485	Sequence 485, App
26	20.8	50.7	1731	US-10-007-693-57	Sequence 57, App
27	20.8	50.7	1731	US-10-007-693-57	Sequence 57, App
28	20.8	50.7	6004	US-08-961-527-87	Sequence 27, App
29	20.8	50.7	6004	US-10-158-844-27	Sequence 27, App
30	20.8	50.7	163701	US-10-322-281-439	Sequence 439, App
31	20.8	50.7	227931	US-10-085-117-274	Sequence 274, App
32	20.8	50.7	123025	US-10-289-762-1	Sequence 1, App
33	20.6	50.2	3849	US-10-094-749-414	Sequence 414, App
34	20.6	50.2	4008	US-10-437-963-47465	Sequence 47465, A
35	20.6	50.2	17203	US-09-864-761-20867	Sequence 20867, A
36	20.6	50.2	17203	US-10-029-386-20814	Sequence 20814, A
37	20.6	50.2	81940	US-09-759-508B-1	Sequence 1, App
38	20.6	50.2	81940	US-09-759-508B-1	Sequence 1092, App
39	20.6	50.2	81940	US-09-873-219-724	Sequence 724, App
40	20.6	50.2	465237	US-09-933-267A-1	Sequence 1, App
41	20.4	49.8	296	US-10-040-739-549	Sequence 549, App
42	20.4	49.8	519	US-10-424-599-138049	Sequence 138049,
43	20.4	49.8	1741	US-10-027-632-98382	Sequence 98382, A
44	20.4	49.8	1741	US-10-027-632-98382	Sequence 98382, A
45	20.4	49.8	1741	US-10-027-632-98382	Sequence 98382, A
46	20.4	49.8	1741	US-10-027-632-98382	Sequence 98382, A
47	20.4	49.8	2151	US-09-814-353-20572	Sequence 20572, A
48	20.4	49.8	2500	US-10-302-172-246	Sequence 246, App
49	20.4	49.8	2117	US-10-190-435-81	Sequence 81, App
50	20.4	49.8	2789	US-10-398-221-3655	Sequence 3655, App
51	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
52	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
53	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
54	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
55	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
56	20.4	49.8	31718	US-09-764-872-812	Sequence 812, App
57	20.4	49.8	202251	US-10-087-192-985	Sequence 985, App
58	20.4	49.8	2940917	US-10-027-632-174763	Sequence 174763,
59	20.2	49.3	2940917	US-10-027-632-174763	Sequence 174763,
60	20.2	49.3	413	US-09-770-423-523	Sequence 523, App
61	20.2	49.3	531	US-10-027-632-77374	Sequence 77374, A
62	20.2	49.3	531	US-10-027-632-77374	Sequence 77374, A
63	20.2	49.3	531	US-10-027-632-77374	Sequence 77374, A
64	20.2	49.3	739	US-10-027-632-17072	Sequence 17072, A
65	20.2	49.3	739	US-10-027-632-17072	Sequence 17072, A
66	20.2	49.3	1014	US-09-891-641-61	Sequence 61, App
67	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
68	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
69	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
70	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
71	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
72	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
73	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
74	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
75	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
76	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
77	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
78	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
79	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
80	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
81	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
82	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
83	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
84	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A
85	20.2	49.3	1014	US-10-369-493-11300	Sequence 41390, A

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 : Search time 37.1814 Seconds
(without alignment) 783.789 Million cell updates/sec

Title: US-10-035-833A-7064

Perfect score: 41

Sequence: 1 tgcagcagctaccacacta.....cttcctcgtatttgatgca 41

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: /cgcn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgcn2_6/prodata/1/ina/5B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20.8	50.7	450	4	US-09-583-110-236
C 2	20.8	50.7	6004	4	US-08-961-527-27
C 3	20.8	50.7	1230025	4	US-09-198-452A-1
C 4	20.6	50.2	469	4	US-09-270-767-5411
C 5	20.6	50.2	469	4	US-09-270-767-20693
C 6	20.4	49.8	734	3	US-09-014-583-1
C 7	20.4	49.8	1667	3	US-08-485-284A-1
C 8	20.4	49.8	2500	4	US-09-799-451-246
C 9	20.2	49.3	1014	4	US-09-891-641-61
C 10	20.2	49.3	1550	3	US-08-943-731-70
C 11	20.2	49.3	38682	3	US-08-943-731-2
C 12	19.8	48.3	213	4	US-09-248-796A-8081
C 13	19.8	48.3	972	4	US-09-134-000C-1431
C 14	19.6	47.8	330	4	US-09-248-796A-10871
C 15	19.6	47.8	503	3	US-09-004-838-134
C 16	19.6	47.8	633	4	US-09-248-796A-4809
C 17	19.6	47.8	918	4	US-09-270-767-2827
C 18	19.6	47.8	918	4	US-09-270-767-18109
C 19	19.6	47.8	1422	4	US-09-248-796A-1632
C 20	19.6	47.8	2247	3	US-08-760-615-5
C 21	19.6	47.8	5552	4	US-09-687-875A-1
C 22	19.6	47.8	13977	4	US-09-484-970B-60
C 23	19.6	47.8	1664976	4	US-08-916-421B-1
C 24	19.6	47.8	1664976	4	US-09-692-570-1
C 25	19.4	47.3	717	4	US-09-496-445-3
C 26	19.4	47.3	782	4	US-09-714-550-8
C 27	19.4	47.3	939	4	US-09-134-000C-1055

C 28	19.4	47.3	2470	4	US-09-270-767-14340	Sequence 14340, A
C 29	19.4	47.3	2479	3	US-09-050-863-4	Sequence 4, Appli
C 30	19.4	47.3	2479	3	US-09-359-081-4	Sequence 4, Appli
C 31	19.4	47.3	2792	4	US-08-994-689C-8	Sequence 8, Appli
C 32	19.4	47.3	3218	4	US-09-496-445-4	Sequence 4, Appli
C 33	19.4	47.3	3318	4	US-08-169-613A-1	Sequence 1, Appli
C 34	19.4	47.3	3944	4	US-07-678-408A-1	Sequence 1, Appli
C 35	19.4	47.3	4069	4	US-09-170-496D-287	Sequence 287, App
C 36	19.4	47.3	4069	4	US-09-170-496D-288	Sequence 288, App
C 37	19.4	47.3	4069	4	US-09-364-425B-52	Sequence 52, Appli
C 38	19.4	47.3	4069	4	US-09-364-425B-53	Sequence 53, Appli
C 39	19.4	47.3	4273	3	US-08-795-430-3	Sequence 3, Appli
C 40	19.4	47.3	4273	3	US-09-355-700-3	Sequence 3, Appli
C 41	19.4	47.3	4273	4	US-08-601-132-37	Sequence 37, Appli
C 42	19.4	47.3	4273	4	US-08-601-132-37	Sequence 37, Appli
C 43	19.4	47.3	4273	4	US-09-631-092B-37	Sequence 37, Appli
C 44	19.4	47.3	4503	3	US-08-675-566-7	Sequence 7, Appli
C 45	19.4	47.3	4810	1	US-08-188-281B-3	Sequence 3, Appli
C 46	19.4	47.3	4810	1	US-08-453-552-7	Sequence 7, Appli
C 47	19.4	47.3	4810	2	US-08-710-637-7	Sequence 7, Appli
C 48	19.4	47.3	4810	5	PCT-US93-00907-7	Sequence 7, Appli
C 49	19.4	47.3	4810	5	PCT-US94-07280-3	Sequence 3, Appli
C 50	19.4	47.3	4810	5	PCT-US95-01087-3	Sequence 3, Appli
C 51	19.4	47.3	5125	1	US-08-453-552-11	Sequence 11, Appli
C 52	19.4	47.3	5125	2	US-08-710-637-11	Sequence 11, Appli
C 53	19.4	47.3	5125	5	PCT-US93-00907-11	Sequence 11, Appli
C 54	19.4	47.3	5157	2	US-08-474-169-7	Sequence 7, Appli
C 55	19.4	47.3	5178	2	US-08-474-169-2	Sequence 2, Appli
C 56	19.4	47.3	5183	3	US-09-039-555B-18	Sequence 18, Appli
C 57	19.4	47.3	5188	1	US-08-123-761A-1	Sequence 1, Appli
C 58	19.4	47.3	5215	4	US-09-173-053-8	Sequence 8, Appli
C 59	19.4	47.3	5233	2	US-08-114-335-2	Sequence 2, Appli
C 60	19.4	47.3	5276	4	US-08-994-689C-9	Sequence 9, Appli
C 61	19.4	47.3	5276	1	US-08-453-552-9	Sequence 9, Appli
C 62	19.4	47.3	5333	2	US-08-710-637-9	Sequence 9, Appli
C 63	19.4	47.3	5333	5	PCT-US93-00907-9	Sequence 9, Appli
C 64	19.4	47.3	5337	2	US-08-784-512-4	Sequence 4, Appli
C 65	19.4	47.3	5337	3	US-09-176-228-4	Sequence 4, Appli
C 66	19.4	47.3	5789	3	US-08-862-431-32	Sequence 32, Appli
C 67	19.4	47.3	5791	3	US-08-862-431-31	Sequence 31, Appli
C 68	19.4	47.3	5793	3	US-08-862-431-29	Sequence 29, Appli
C 69	19.4	47.3	5793	3	US-08-862-431-30	Sequence 30, Appli
C 70	19.4	47.3	5818	2	US-08-536-559A-2	Sequence 2, Appli
C 71	19.4	47.3	5819	2	US-08-536-559A-2	Sequence 2, Appli
C 72	19.4	47.3	5819	3	US-08-862-431-27	Sequence 27, Appli
C 73	19.4	47.3	5819	3	US-08-862-431-28	Sequence 28, Appli
C 74	19.4	47.3	5825	4	US-08-809-513A-7	Sequence 7, Appli
C 75	19.4	47.3	5916	4	US-09-826-630-9	Sequence 9, Appli
C 76	19.4	47.3	5938	2	US-08-536-559A-4	Sequence 4, Appli
C 77	19.4	47.3	6092	2	US-08-536-559A-1	Sequence 1, Appli
C 78	19.4	47.3	6092	3	US-08-862-431-26	Sequence 26, Appli
C 79	19.4	47.3	6151	5	PCT-US91-02934-12	Sequence 12, Appli
C 80	19.4	47.3	6206	2	US-08-474-169-3	Sequence 3, Appli
C 81	19.4	47.3	6240	1	US-08-374-483-1	Sequence 1, Appli
C 82	19.4	47.3	6601	2	US-08-232-463-15	Sequence 15, Appli
C 83	19.4	47.3	6603	2	US-08-244-434-36	Sequence 36, Appli
C 84	19.4	47.3	6630	2	US-08-244-434-37	Sequence 37, Appli
C 85	19.4	47.3	7000	4	US-09-714-550-18	Sequence 18, Appli
C 86	19.4	47.3	7218	1	US-08-232-463-14	Sequence 14, Appli
C 87	19.4	47.3	7453	2	US-08-715-808-13	Sequence 13, Appli
C 88	19.4	47.3	7721	4	US-09-301-593-42	Sequence 42, Appli
C 89	19.4	47.3	7731	4	US-09-301-593-42	Sequence 42, Appli
C 90	19.4	47.3	7882	2	US-07-916-098A-40	Sequence 40, Appli
C 91	19.4	47.3	7882	2	US-07-916-098A-40	Sequence 40, Appli
C 92	19.4	47.3	8068	4	US-09-301-593-27	Sequence 27, Appli
C 93	19.4	47.3	8068	4	US-09-301-593-35	Sequence 35, Appli
C 94	19.4	47.3	8068	1	US-08-652-859A-6	Sequence 6, Appli
C 95	19.4	47.3	8511	1	US-08-462-859A-8	Sequence 8, Appli
C 96	19.4	47.3	8511	1	US-08-123-659A-6	Sequence 6, Appli
C 97	19.4	47.3	8511	1	US-08-123-659A-8	Sequence 8, Appli
C 98	19.4	47.3	8511	1	US-08-464-247A-6	Sequence 6, Appli
C 99	19.4	47.3	8581	1	US-08-464-247A-8	Sequence 8, Appli
C 100	19.4	47.3	8581	1	US-08-464-248A-6	Sequence 6, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:35:05 ; Search time 177.265 seconds
(without alignments)
1214.152 Million cell updates/sec

Title: US-10-035-833a-7064
Perfect score: 41
Sequence: 1 tgcagacactcaccaccta.....ttcctctgatttgcgtca 41

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 413486 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.6	99.0	41	6	ABZ50282 Human CYC
2	40.6	99.0	41	6	ABZ44455 Human CYC
3	31.4	76.6	5735	6	ABK40066 Human CHE
4	23	56.1	5735	6	ABK40065 Human CHE
5	22.2	54.1	470	6	AAS31566 Human DNA
6	22.2	54.1	470	6	ABO66890 Human DNA
7	22.2	54.1	470	10	ADCI1177 Human DNA
8	21.6	53.2	9046	4	AAK87480 Human IMM
9	21.6	52.7	721	4	AAI94863 Human NEU
10	21.6	52.7	873	4	AAH07369 Human CDN
11	21.6	52.7	1728	4	AAH14783 Human CDN
12	21.6	52.7	2733	3	AAZ57852 Protein X
13	21.6	52.7	2733	5	AAS80660 DNA encod
14	21.6	52.7	4237	10	ADP82137 Leukemia
15	21.2	51.7	567	4	AAK92572 Human CDN
16	21.2	51.7	567	4	AAK94075 Human CDN
17	21.2	51.7	567	12	ADL28999 3' end of
18	21.2	51.7	567	12	ADL30502 3' end of
19	21.2	51.7	1488	4	ABL1559 Drosophila
20	21.2	51.7	4003	4	ABL1558 Drosophila
21	21.2	51.7	80374	12	ADM88956 Diterpene

22	51.2	1278	10	ACF70673	AcF70673 Phototax
23	51.2	32404	9	ADA02894	Ada02894 Human BLR
24	51.2	32404	10	ADB72632	ADB72632 Human BLR
25	51.2	32404	10	ADC85373	ADC85373 Mouse BLR
26	51.2	32404	12	ADM74489	ADM74489 Human car
27	51.2	110000	10	ACF67367	ACF67367 Streptoc
28	51.2	110000	10	ACF65388	ACF65388 Streptoc
29	50.7	587	2	AAV42942	AAV42942 Streptoc
30	50.7	1731	2	AAV57025	AAV57025 C. pneumo
31	50.7	1731	6	ABL92668	ABL92668 Chlamydia
32	50.7	1731	10	ADD42819	ADD42819 Chlamydia
33	50.7	6004	2	AAV52160	AAV52160 Streptoc
34	50.7	8489	4	ABLI6018	ABLI6018 Drosophila
35	50.7	110000	2	AAK19990	AAK19990 Nucleotid
36	50.7	110000	10	ABZ56454	ABZ56454 Continuation (5 of
37	50.2	705	10	ADK54621	ADK54621 Plant DNA
38	50.2	831	4	AAK93836	AAK93836 Human CDN
39	50.2	831	4	AAK91673	AAK91673 Human CDN
40	50.2	831	12	ADL30263	ADL30263 3' end of
41	50.2	1133	12	ADM95343	ADM95343 Novel full
42	50.2	2375	4	AAK94180	AAK94180 Novel full
43	50.2	2375	12	ADL30689	ADL30689 Novel full
44	50.2	2548	5	ADM19592	ADM19592 Novel hum
45	50.2	2743	5	AAK76597	AAK76597 DNA encod
46	50.2	3849	10	ADA52846	ADA52846 Human cod
47	50.2	4124	4	ABLI03432	ABLI03432 Drosophila
48	50.2	4359	4	ABLI9258	ABLI9258 Drosophila
49	50.2	17203	4	ABA68567	ABA68567 Probe #14
50	50.2	17203	4	ABA65547	ABA65547 Human bon
51	50.2	17203	4	AAK42707	AAK42707 Human bra
52	50.2	17203	4	AAK16933	AAK16933 Human liv
53	50.2	17203	5	AAI09088	AAI09088 Probe #90
54	50.2	17203	12	ACH87619	ACH87619 Human gen
55	50.2	17203	4	AAK05390	AAK05390 Human ben
56	50.2	81940	6	ABK64829	ABK64829 Human sof
57	50.2	81940	12	ADQ17315	ADQ17315 Human RGS
58	50.2	81940	9	ABX13540	ABX13540 Human oes
59	50.2	93801	6	ABA90193	ABA90193 Human oes
60	50.2	110000	6	ABO87681	ABO87681 Human oes
61	50.2	110000	6	ABO87681	ABO87681 Gene enco
62	50.2	110000	8	ABX37717	ABX37717 Human gen
63	50.2	110000	2	AAI25304	AAI25304 EST clone
64	49.8	294	2	AAV88071	AAV88071 Human sig
65	49.8	296	3	AAZ98110	AAZ98110 Nucleotid
66	49.8	706	3	AAK61150	AAK61150 Human sec
67	49.8	1667	2	AAQ46589	AAQ46589 Human ova
68	49.8	1879	5	ADL62360	ADL62360 Human pol
69	49.8	2151	5	ABZ11364	ABZ11364 Human pol
70	49.8	2500	12	ADM43882	ADM43882 Novel hum
71	49.8	2500	12	ADM43882	ADM43882 Novel hum
72	49.8	2717	10	ADCI1302	ADCI1302 DNA of Hi
73	49.8	2789	12	ADH56194	ADH56194 Arabinidops
74	49.8	3246	12	ADH56192	ADH56192 Arabinidops
75	49.8	3246	12	ADH56192	ADH56192 Arabinidops
76	49.8	3718	4	AAK90359	AAK90359 Human dig
77	49.8	3718	4	AAK90360	AAK90360 Human dig
78	49.8	3718	4	AAK87573	AAK87573 Human imm
79	49.8	3718	4	AAK73104	AAK73104 Human imm
80	49.8	3718	4	AAK875120	AAK875120 Human imm
81	49.8	3718	4	AAK87443	AAK87443 Human imm
82	49.8	3718	4	AAK87592	AAK87592 Human rep
83	49.8	3718	4	AAK87592	AAK87592 Human rep
84	49.8	3718	4	AAK87592	AAK87592 Human rep
85	49.8	3718	4	AAK87592	AAK87592 Human rep
86	49.8	3718	4	AAK87592	AAK87592 Human rep
87	49.8	3718	4	AAK87592	AAK87592 Human rep
88	49.8	3718	4	AAK87592	AAK87592 Human rep
89	49.8	3718	4	AAK87592	AAK87592 Human rep
90	49.8	3718	4	AAK87592	AAK87592 Human rep
91	49.8	3718	4	AAK87592	AAK87592 Human rep
92	49.8	3718	4	AAK87592	AAK87592 Human rep
93	49.8	3718	4	AAK87592	AAK87592 Human rep
94	49.3	413	8	ABX62408	ABX62408 Arabinidops

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 04:40:10 ; Search time 720.113 Seconds
(without alignments)
2692.466 Million cell updates/sec

Title: US-10-035-833a-7064

Perfect score: 41
Sequence: 1 tgcagcactaccaccta.....ttccctcgtatttgatca 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: gb_ba:*
2: gb_neg:*
3: gb_in:*
4: gb_om:*
5: gb_cv:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_yi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.6	99.0	41	6	AXS15041 Sequence
2	40.6	99.0	41	6	AXS20866 Sequence
3	40.6	99.0	79303	2	AXS101074 Homo sapi
4	40.6	99.0	209156	9	AC0093229 Homo sapi
5	40.6	99.0	211222	2	AC0022097 Homo sapi
6	31.4	76.6	5735	6	AX348453 Sequence
7	24.6	60.0	229045	9	AC008680 Homo sapi
8	24.6	60.0	236365	2	AC087099 Mus muscu
9	24.2	59.0	151506	8	OSJN00080 Oryza sat
10	24.2	59.0	156077	9	AL354997 Human DNA
11	24.2	59.0	165745	8	OSJN00105 Oryza sat
12	24.2	59.0	228427	10	AC107738 Mus muscu
13	23.8	58.0	262288	2	AC103137 Rattus no
14	23.8	58.0	263283	2	AC109389 Rattus no
15	23.6	57.6	164221	2	AC148133 Ateleiex
16	23.6	57.6	227579	2	AC150579 Bos tauru
17	23.4	57.1	124518	9	AL138962 Human DNA
18	23.4	57.1	136155	10	AC132586 Mus muscu
19	23.4	57.1	174426	10	AC145504 Mus muscu
20	23.4	57.1	180516	10	AC122442 Mus muscu
21	23.4	57.1	180602	10	AC134429 Mus muscu
22	23.4	57.1	211871	10	AL672306 Mouse DNA
23	23.4	57.1	215319	2	AC099473 Rattus no
24	23.4	57.1	218270	2	AC079499 Mus muscu
25	23.4	57.1	224373	2	AC098129 Rattus no
26	23.4	57.1	240482	2	AC122975 Rattus no
27	23.4	57.1	347664	10	BX863043 Rattus no
28	23.2	56.6	223200	2	AC109959 Rattus no
29	23.2	56.6	249667	2	AC114720 Rattus no
30	23.2	56.6	277490	2	AC097085 Rattus no
31	23	56.1	5735	6	AX348452 Sequence
32	23	56.1	63352	2	AC110047 Homo sapi
33	23	56.1	67822	2	AC027792 Homo sapi
34	23	56.1	129285	5	AC091726 Gallus ga
35	23	56.1	157081	2	AC023084 Homo sapi
36	23	56.1	161842	2	AC107931 Homo sapi
37	23	56.1	162066	9	AC018989 Homo sapi
38	23	56.1	173693	2	AC142422 Rattus no
39	23	56.1	174152	10	AC132133 Mus muscu
40	23	56.1	176643	9	AC005324 Homo sapi
41	23	56.1	197470	2	AC026964 Homo sapi
42	23	56.1	203810	10	AC132612 Mus muscu
43	23	56.1	247189	2	AC109910 Rattus no
44	23	56.1	251589	2	AC111900 Rattus no
45	23	56.1	258648	2	AC130010 Rattus no
46	23	56.1	311823	2	AC095362 Rattus no
47	22.8	55.6	110000	4	AC107201-4 Continuation (5 of
48	22.8	55.6	118504	9	AC094080 Homo sapi
49	22.8	55.6	133054	10	AC107447 Rattus no
50	22.8	55.6	150528	9	AC010260 Homo sapi
51	22.8	55.6	152838	2	AC011589 Homo sapi
52	22.8	55.6	170797	9	AC011379 Homo sapi
53	22.8	55.6	208764	10	AC098875 Mus muscu
54	22.8	55.6	210675	2	AC026272 Homo sapi
55	22.8	55.6	211034	10	AL731709 Mouse DNA
56	22.8	55.6	218170	10	AC102119 Mus muscu
57	22.8	55.6	225342	2	AC132765 Rattus no
58	22.8	55.6	231155	2	AC123664 Mus muscu
59	22.8	55.6	243640	2	AC108571 Rattus no
60	22.8	55.6	256020	2	AC115250 Rattus no
61	22.8	55.6	275059	2	AC120776 Rattus no
62	22.6	55.1	81019	2	AC149536 Xenopus t
63	22.6	55.1	93010	10	AL627386 Mouse DNA
64	22.6	55.1	113715	2	AC149149 Xenopus t
65	22.6	55.1	134066	2	AC146759 Mus muscu
66	22.6	55.1	180485	2	AC027145 Homo sapi
67	22.6	55.1	180725	2	AC119511 Rattus no
68	22.6	55.1	196755	2	AC140779 Mus muscu
69	22.6	55.1	210562	2	AC134489 Rattus no
70	22.6	55.1	227996	2	AC117916 Rattus no
71	22.6	55.1	234859	2	AC128112 Rattus no
72	22.6	55.1	247577	2	AC106830 Rattus no
73	22.6	55.1	261708	2	AC098350 Rattus no
74	22.6	55.1	282849	2	AC132855 Rattus no
75	22.6	54.6	69337	2	AC101261 Mus muscu
76	22.4	54.6	140575	8	AP005502 Oryza sat
77	22.4	54.6	146473	2	AC149883 Xenopus t
78	22.4	54.6	166272	8	AP004634 Oryza sat
79	22.4	54.6	168199	10	AC131794 Mus muscu
80	22.4	54.6	168380	2	AC116042 Papio ham
81	22.4	54.6	179454	2	AC123737 Mus muscu
82	22.4	54.6	181442	10	AC114917 Mus muscu
83	22.4	54.6	184634	2	AC115359 Mus muscu
84	22.4	54.6	185027	2	AC123234 Rattus no
85	22.4	54.6	210148	10	AL928791 Mouse DNA
86	22.4	54.6	236247	2	AC123009 Rattus no
87	22.4	54.6	265537	2	AC087228 Mus muscu
88	22.4	54.1	29682	2	AC012638 Homo sapi
89	22.2	54.1	93511	9	BX927132 Human DNA
90	22.2	54.1	102196	9	CR388415 Human DNA

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2004, 08:13:20 ; Search time 37.1814 Seconds
(without alignments)
783.789 Million cell updates/sec

Title: US-10-035-833A-7063

Perfect score: 41
Sequence: 1 tgcattccgtgaagcaccac.....gtatccctctctgcacatg 41

Scoring table: IDENTITY NUC
Gapox 10.0 ; Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.8	50.7	38584	3	US-09-453-702B-50
2	20.6	50.2	43	1	US-08-403-762A-84
3	20.6	50.2	43	1	US-08-403-762A-88
4	20.2	49.3	44	1	US-08-403-762A-87
5	20.2	49.3	2431	3	US-08-985-526-35
6	20.2	49.3	5406	1	US-07-813-593-3
7	20.2	49.3	5406	1	US-07-977-451-5
8	20.2	49.3	5406	1	US-07-946-507-3
9	20.2	49.3	5406	1	US-08-252-517-5
10	20.2	49.3	5406	1	US-07-906-397A-5
11	20.2	49.3	5406	1	US-08-601-891-5
12	20.2	49.3	5406	2	US-09-021-324-5
13	20.2	49.3	5406	2	US-09-872-136B-5
14	20.2	49.3	5406	5	PCT-US92-02750-7
15	20.2	49.3	5406	5	PCT-US92-05401-5
16	20.2	49.3	5406	5	PCT-US92-09893-5
17	20.2	49.3	5470	2	US-08-443-861-1
18	20.2	49.3	5470	2	US-08-193-829B-1
19	20.2	49.3	5470	4	US-09-967-655-10
20	20.2	49.3	415	4	US-09-513-993C-16647
21	20	48.8	1281	4	US-09-270-767-10191
22	20	48.8	4381	3	US-09-147-878-19
23	20	48.8	9626	4	US-09-150-867-2
24	19.8	48.3	366	1	US-08-318-970B-32
25	19.8	48.3	407	4	US-09-621-976-17495
26	19.8	48.3	438	1	US-08-318-970B-42
27	19.8	48.3	687	4	US-09-248-796A-6341

C	28	19.8	48.3	2621	2	US-08-553-619B-8	Sequence 8, Appli
	29	19.8	47.8	44453	1	US-09-146-053-5	Sequence 5, Appli
	30	19.6	47.8	43	1	US-08-403-762A-90	Sequence 90, Appl
	31	19.6	47.8	43	1	US-08-403-762A-91	Sequence 91, Appl
	32	19.6	47.8	2606	3	US-09-252-816A-7	Sequence 7, Appli
	33	19.6	47.8	2606	4	US-09-837-654-7	Sequence 1, Appli
	34	19.6	47.8	3100	1	US-08-296-362-1	Sequence 6, Appli
	35	19.6	47.8	3439	3	US-09-252-816A-6	Sequence 6, Appli
	36	19.6	47.8	3439	3	US-09-837-654-6	Sequence 73, Appl
	37	19.4	47.3	372	4	US-09-240-274-73	Sequence 19, Appl
	38	19.4	47.3	372	4	US-08-844-215-17	Sequence 17, Appl
	39	19.4	47.3	35828	3	US-09-449-218D-17	Sequence 17, Appl
	40	19.4	47.3	35828	4	US-09-668-529A-17	Sequence 17, Appl
	41	19.4	47.3	35828	4	US-09-668-037A-17	Sequence 11, Appl
	42	19.2	46.8	486	4	US-09-817-318-11	Sequence 15, Appl
	43	19.2	46.8	732	3	US-09-437-054A-15	Sequence 26, Appl
	44	19.2	46.8	1294	4	US-09-904-615-26	Sequence 191, Ap
	45	19.2	46.8	1973	4	US-09-016-434-1391	Sequence 1417, Ap
	46	19.2	46.8	1973	4	US-09-023-655-1417	Sequence 1, Appli
	47	19.2	46.8	4345	2	US-08-244-537-1	Sequence 5, Appli
	48	19.2	46.8	7470	3	US-08-417-089-5	Sequence 5, Appli
	49	19.2	46.8	7470	3	US-08-695-651-5	Sequence 5, Appli
	50	19.2	46.8	7470	3	US-08-930-285-5	Sequence 5, Appli
	51	19.2	46.8	7470	3	US-08-695-421-5	Sequence 5, Appli
	52	19.2	46.8	7470	3	US-08-697-826A-9	Sequence 5, Appli
	53	19	46.3	76	1	US-08-009-265-15	Sequence 15, Appl
	54	19	46.3	192	2	US-08-822-028-63	Sequence 63, Appl
	55	19	46.3	192	3	US-08-479-285-63	Sequence 63, Appl
	56	19	46.3	192	4	US-09-503-653A-63	Sequence 462, App
	57	19	46.3	417	4	US-09-320-352-482	Sequence 13128, A
	58	19	46.3	807	4	US-09-270-767-1128	Sequence 1, Appli
	59	19	46.3	1008	4	US-09-780-641-1	Sequence 4, Appli
	60	19	46.3	2310	1	US-08-261-822A-4	Sequence 4, Appli
	61	19	46.3	2310	5	PCT-US95-07744A-4	Sequence 4, Appli
	62	19	46.3	3387	1	US-08-261-822A-5	Sequence 5, Appli
	63	19	46.3	3387	5	PCT-US95-07744A-5	Sequence 75, Appli
	64	19	46.3	3586	4	US-09-631-594-75	Sequence 5, Appli
	65	19	46.3	1168	4	US-09-434-840-5	Sequence 8, Appli
	66	18.8	45.9	947	4	US-09-673-395A-8	Sequence 289, App
	67	18.8	45.9	1001	4	US-09-671-317-289	Sequence 123, App
	68	18.8	45.9	1258	3	US-08-936-165A-123	Sequence 1171, Ap
	69	18.8	45.9	1930	4	US-09-016-434-1171	Sequence 1, Appli
	70	18.8	45.9	2163	3	US-09-186-276B-1	Sequence 1, Appli
	71	18.8	45.9	2163	4	US-09-842-445-1	Sequence 1, Appli
	72	18.8	45.9	2163	4	US-09-186-168B-1	Sequence 1, Appli
	73	18.8	45.9	5475	2	US-08-680-327-1	Sequence 1, Appli
	74	18.8	45.9	5475	2	US-09-228-245-3	Sequence 2, Appli
	75	18.8	45.9	10968	2	US-08-680-327-2	Sequence 1, Appli
	76	18.8	45.9	10968	4	US-09-228-245-1	Sequence 38, Appl
	77	18.8	45.9	23439	4	US-08-956-171E-38	Sequence 2329, Ap
	78	18.8	45.9	318	4	US-08-781-986A-18	Sequence 3682, Ap
	79	18.6	45.4	414	4	US-08-956-171E-3882	Sequence 668, App
	80	18.6	45.4	414	4	US-08-781-986A-18682	Sequence 36, Appl
	81	18.6	45.4	659	3	US-09-328-11-668	Sequence 843, App
	82	18.6	45.4	1080	4	US-09-646-028-39	Sequence 38, Appl
	83	18.6	45.4	1086	4	US-09-646-028-36	Sequence 304, App
	84	18.6	45.4	1105	4	US-09-646-028-36	Sequence 1230, Ap
	85	18.6	45.4	1105	4	US-09-016-434-843	Sequence 16, Appl
	86	18.6	45.4	1737	4	US-09-646-028-38	Sequence 16, Appl
	87	18.6	45.4	1757	4	US-09-554-560-3	Sequence 16, Appl
	88	18.6	45.4	2184	3	US-09-134-001C-1230	Sequence 16, Appl
	89	18.6	45.4	2226	2	US-08-999-849B-16	Sequence 16, Appl
	90	18.6	45.4	2226	2	US-08-142-368B-16	Sequence 16, Appl
	91	18.6	45.4	2226	3	US-08-967-727-16	Sequence 16, Appl
	92	18.6	45.4	2226	3	US-08-037-230D-16	Sequence 16, Appl
	93	18.6	45.4	2226	4	US-09-583-850-16	Sequence 16, Appl
	94	18.6	45.4	2226	4	US-09-579-197-16	Sequence 16, Appl
	95	18.6	45.4	2226	4	US-09-404-026-16	Sequence 16, Appl
	96	18.6	45.4	2226	4	US-09-312-464-16	Sequence 16, Appl
	97	18.6	45.4	2305	1	US-08-299-849B-17	Sequence 17, Appl
	98	18.6	45.4	2305	1	US-08-142-368B-17	Sequence 17, Appl
	99	18.6	45.4	2305	3	US-08-567-727-17	Sequence 17, Appl
	100	18.6	45.4	2305	3	US-08-567-727-17	Sequence 17, Appl